



# 8

SEQUENCE LISTING

# 8

<110> Ole THASTRUP  
Sara BJRON  
Soren TULLIN  
Kasper ALMHOLT  
Kurt SCUDDER

<120> A Method For Extracting Quantitative Information Relating To An  
Influence On A Cellular Response

<130> 3759-0120P

<140> 10/072,036  
<141> 2002-02-05

<150> 09/417,197

<151> 1999-10-07

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<170> PatentIn version 3.0

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Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1			5					10					15			
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
			50			55					60					
ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
					70				75					80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90						95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	



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Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc			528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser			
165	170	175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc			576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly			
180	185	190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg			624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu			
195	200	205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc			672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe			
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Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser			
225	230	235	240
gga ctc aga tct cga gct caa gct tcg aat tca acc atg gcg gcg gcg			768
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ala Ala Ala			
245	250	255	
gcg gct cag ggg ggc ggg ggc ggg gag ccc cgt aga acc gag ggg gtc			816
Ala Ala Gln Gly Gly Gly Gly Gly Glu Pro Arg Arg Thr Glu Gly Val			
260	265	270	
ggc ccg ggg gtc ccg ggg gag gtg gag atg gtg aag ggg cag ccg ttc			864
Gly Pro Gly Val Pro Gly Glu Val Glu Met Val Lys Gly Gln Pro Phe			
275	280	285	
gac gtg ggc ccg cgc tac acg cag ttg cag tac atc ggc gag ggc gcg			912
Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr Ile Gly Glu Gly Ala			
290	295	300	
tac ggc atg gtc agc tcg gcc tat gac cac gtg cgc aag act cgc gtg			960
Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val Arg Lys Thr Arg Val			
305	310	315	320
gcc atc aag aag atc agc ccc ttc gaa cat cag acc tac tgc cag cgc			1008
Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln Arg			
325	330	335	
acg ctc cgg gag atc cag atc ctg ctg cgc ttc cgc cat gag aat gtc			1056
Thr Leu Arg Glu Ile Gln Ile Leu Arg Phe Arg His Glu Asn Val			
340	345	350	
atc ggc atc cga gac att ctg cgg gcg tcc acc ctg gaa gcc atg aga			1104
Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala Met Arg			
355	360	365	
gat gtc tac att gtg cag gac ctg atg gag act gac ctg tac aag ttg			1152
Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys Leu			
370	375	380	
ctg aaa agc cag cag ctg agc aat gac cat atc tgc tac ttc ctc tac			1200
Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe Leu Tyr			
385	390	395	400
cag atc ctg cgg ggc ctc aag tac atc cac tcc gcc aac gtg ctc cac			1248
Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu His			
405	410	415	
cga gat cta aag ccc tcc aac ctg ctc agc aac acc acc tgc gac ctt			1296
Arg Asp Leu Lys Pro Ser Asn Leu Leu Ser Asn Thr Thr Cys Asp Leu			
420	425	430	
aag att tgt gat ttc ggc ctg gcc cgg att gcc gat cct gag cat gac			1344
Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu His Asp			
435	440	445	
cac acc ggc ttc ctg acg gag tat gtg gct acg cgc tgg tac cgg gcc			1392
His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala			
450	455	460	
cca gag atc atg ctg aac tcc aag ggc tat acc aag tcc atc gac atc			1440
Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp Ile			

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Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro Ile							
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Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly Ile							
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ctg ggc tcc cca tcc cag gag gac ctg aat tgt atc atc aac atg aag							1584
Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn Met Lys							
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gcc cga aac tac cta cag tct ctg ccc tcc aag acc aag gtg gct tgg							1632
Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val Ala Trp							
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gcc aag ctt ttc ccc aag tca gac tcc aaa gcc ctt gac ctg ctg gac							1680
Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu Leu Asp							
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cgg atg tta acc ttt aac ccc aat aaa cgg atc aca gtg gag gaa gcg							1728
Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu Glu Ala							
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ctg gct cac ccc tac ctg gag cag tac tat gac ccg acg gat gag cca							1776
Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp Glu Pro							
	580		585			590	
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Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro							
	595		600			605	
aag gag cgg ctg aag gag ctc atc ttc cag gag aca gca cgc ttc cag							1872
Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln							
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35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125  
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140  
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
145 150 155 160  
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175  
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190  
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
195 200 205  
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220  
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
225 230 235 240  
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Thr Met Ala Ala Ala  
245 250 255  
Ala Ala Gln Gly Gly Gly Gly Gly Glu Pro Arg Arg Thr Glu Gly Val  
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275 280 285  
Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr Ile Gly Glu Gly Ala  
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Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys Gln Arg  
325 330 335  
Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe Arg His Glu Asn Val  
340 345 350  
Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala Met Arg  
355 360 365  
Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr Lys Leu  
370 375 380  
Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe Leu Tyr  
385 390 395 400  
Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Leu His  
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Arg Asp Leu Lys Pro Ser Asn Leu Leu Ser Asn Thr Thr Cys Asp Leu  
420 425 430  
Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu His Asp  
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His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr Arg Ala  
450 455 460  
Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile Asp Ile  
465 470 475 480  
Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg Pro Ile  
485 490 495  
Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu Gly Ile  
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515 520 525  
Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val Ala Trp  
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Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu Leu Asp  
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Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu Glu Ala  
565 570 575  
Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp Glu Pro  
580 585 590  
Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp Leu Pro  
595 600 605  
Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg Phe Gln

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Pro Gly Val Leu Glu Ala Pro  
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<223> EGFP-Erk2 fusion

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag      240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc      576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly

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agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
	210					215					220					
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Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225				230						235				240	
gga	ctc	aga	tct	cga	gta	acc	atg	gcg	gcg	gcg	gcg	gcg	gcg	ggc	ccg	768
Gly	Leu	Arg	Ser	Arg	Val	Thr	Met	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Pro	
			245					250						255		
gag	atg	gtc	cgc	ggg	cag	gtg	ttc	gac	gtg	ggg	ccg	cgc	tac	act	aat	816
Glu	Met	Val	Arg	Gly	Gln	Val	Phe	Asp	Val	Gly	Pro	Arg	Tyr	Thr	Asn	
		260						265					270			
ctc	tcg	tac	atc	gga	gaa	ggc	gcc	tac	ggc	atg	gtt	tgt	tct	gct	tat	864
Leu	Ser	Tyr	Ile	Gly	Glu	Gly	Ala	Tyr	Gly	Met	Val	Cys	Ser	Ala	Tyr	
	275						280						285			
gat	aat	ctc	aac	aaa	gtt	cga	gtt	gct	atc	aag	aaa	atc	agt	cct	ttt	912
Asp	Asn	Leu	Asn	Lys	Val	Arg	Val	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe	
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Glu	His	Gln	Thr	Tyr	Cys	Gln	Arg	Thr	Leu	Arg	Glu	Ile	Lys	Ile	Leu	
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ctg	cgc	ttc	aga	cat	gag	aac	atc	atc	ggc	atc	aat	gac	atc	atc	cgg	1008
Leu	Arg	Phe	Arg	His	Glu	Asn	Ile	Ile	Gly	Ile	Asn	Asp	Ile	Ile	Arg	
			325						330					335		
gca	cca	acc	att	gag	cag	atg	aaa	gat	gta	tat	ata	gta	cag	gac	ctc	1056
Ala	Pro	Thr	Ile	Glu	Gln	Met	Lys	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	
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Met	Glu	Thr	Asp	Leu	Tyr	Lys	Leu	Lys	Thr	Gln	His	Leu	Ser	Asn		
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Ile	His	Ser	Ala	Asn	Val	Leu	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	
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Arg	Val	Ala	Asp	Pro	Asp	His	Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	
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Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	
		435					440					445				
ggt	tat	acc	aag	tcc	att	gat	att	tgg	tct	gtg	ggc	tgc	atc	ctg	gca	1392
Gly	Tyr	Thr	Lys	Ser	Ile	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	
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cag	ctg	aat	cac	atc	ctg	ggt	att	ctt	gga	tct	cca	tca	cag	gaa	gat	1488
Gln	Leu	Asn	His	Ile	Leu	Gly	Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	
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ctg	aat	tgt	ata	ata	aat	tta	aaa	gct	aga	aac	tat	ttg	ctt	tct	ctc	1536
Leu	Asn	Cys	Ile	Ile	Asn	Leu	Lys	Ala	Arg	Asn	Tyr	Leu	Leu	Ser	Leu	
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ccg	cac	aaa	aat	aag	gtg	ccg	tgg	aac	agg	ttg	ttc	cca	aac	gct	gac	1584
Pro	His	Lys	Asn	Lys	Val	Pro	Trp	Asn	Arg	Leu	Phe	Pro	Asn	Ala	Asp	

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Ser	Lys	Ala	Leu	Asp	Leu	Leu	Asp
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Lys	Arg	Ile	Glu	Val	Glu	Gln	Ala
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tat	tat	gac	cca	agt	gat	gag	ccc
Tyr	Tyr	Asp	Pro	Ser	Asp	Glu	Pro
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gac	atg	gag	ctg	gac	gac	tta	cct
Asp	Met	Glu	Leu	Asp	Asp	Leu	Pro
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ttt	gaa	gag	act	gct	cga	ttc	cag
Phe	Glu	Glu	Thr	Ala	Arg	Phe	Gln
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<223> EGFP-Erk2 fusion

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Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
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Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
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Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
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Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
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Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
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Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
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Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
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Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
			165					170					175		
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
	180						185					190			
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
	195					200					205				
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
	210					215					220				

Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
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Gly	Leu	Arg	Ser	Arg	Val	Thr	Met	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Pro
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Glu	Met	Val	Arg	Gly	Gln	Val	Phe	Asp	Val	Gly	Pro	Arg	Tyr	Thr	Asn
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Leu	Ser	Tyr	Ile	Gly	Glu	Gly	Ala	Tyr	Gly	Met	Val	Cys	Ser	Ala	Tyr
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Asp	Asn	Leu	Asn	Lys	Val	Arg	Val	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe
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Glu	His	Gln	Thr	Tyr	Cys	Gln	Arg	Thr	Leu	Arg	Glu	Ile	Lys	Ile	Leu
305					310					315					320
Leu	Arg	Phe	Arg	His	Glu	Asn	Ile	Ile	Gly	Ile	Asn	Asp	Ile	Ile	Arg
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Ala	Pro	Thr	Ile	Glu	Gln	Met	Lys	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu
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Met	Glu	Thr	Asp	Leu	Tyr	Lys	Leu	Leu	Lys	Thr	Gln	His	Leu	Ser	Asn
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Asp	His	Ile	Cys	Tyr	Phe	Leu	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr
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Ile	His	Ser	Ala	Asn	Val	Leu	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu
385				390						395					400
Leu	Leu	Asn	Thr	Thr	Cys	Asp	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala
			405						410					415	
Arg	Val	Ala	Asp	Pro	Asp	His	Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr
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Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys
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Gly	Tyr	Thr	Lys	Ser	Ile	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala
		450				455					460				
Glu	Met	Leu	Ser	Asn	Arg	Pro	Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp
465				470						475					480
Gln	Leu	Asn	His	Ile	Leu	Gly	Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp
			485						490					495	
Leu	Asn	Cys	Ile	Ile	Asn	Leu	Lys	Ala	Arg	Asn	Tyr	Leu	Leu	Ser	Leu
			500					505					510		
Pro	His	Lys	Asn	Lys	Val	Pro	Trp	Asn	Arg	Leu	Phe	Pro	Asn	Ala	Asp
			515				520					525			
Ser	Lys	Ala	Leu	Asp	Leu	Leu	Asp	Lys	Met	Leu	Thr	Phe	Asn	Pro	His
		530				535					540				
Lys	Arg	Ile	Glu	Val	Glu	Gln	Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln
545					550					555					560
Tyr	Tyr	Asp	Pro	Ser	Asp	Glu	Pro	Ile	Ala	Glu	Ala	Pro	Phe	Lys	Phe
			565						570					575	
Asp	Met	Glu	Leu	Asp	Asp	Leu	Pro	Lys	Glu	Lys	Leu	Lys	Glu	Leu	Ile
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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20      25      30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35      40      45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50      55      60
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag      240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65      70      75      80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85      90      95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100      105      110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115      120      125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130      135      140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145      150      155      160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165      170      175
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc      576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180      185      190
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg      624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195      200      205
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc      672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210      215      220
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc      720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225      230      235      240
gga ctc aga tct cga gct caa gct tcg aat tcg tca atg gag ctg gaa      768
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ser Met Glu Leu Glu
245      250      255
aac atc gtg gcc aac acg gtc ttg ctg aaa gcc agg gaa ggg ggc gga      816
Asn Ile Val Ala Asn Thr Val Leu Leu Lys Ala Arg Glu Gly Gly Gly
260      265      270
gga aag cgc aaa ggg aaa agc aag tgg aaa gaa atc ctg aag ttc      864
Gly Lys Arg Lys Gly Lys Ser Lys Lys Trp Lys Glu Ile Leu Lys Phe
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	290					295					300					
tac	tgc	agt	tta	tgt	gac	aag	cag	cca	atc	ggg	agg	ctg	ctt	ttc	cgg	960
Tyr	Cys	Ser	Leu	Cys	Asp	Lys	Gln	Pro	Ile	Gly	Arg	Leu	Leu	Phe	Arg	
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Gln	Phe	Cys	Glu	Thr	Arg	Pro	Gly	Leu	Glu	Cys	Tyr	Ile	Gln	Phe	Leu	
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Lys	Gly	Lys	Glu	Ile	Met	Thr	Lys	Tyr	Leu	Thr	Pro	Lys	Ser	Pro	Val	
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Phe	Ile	Ala	Gln	Val	Gly	Gln	Asp	Leu	Val	Ser	Gln	Thr	Glu	Glu	Lys	
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Leu	Leu	Gln	Lys	Pro	Cys	Lys	Glu	Leu	Phe	Ser	Ala	Cys	Ala	Gln	Ser	
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Val	His	Glu	Tyr	Leu	Arg	Gly	Glu	Pro	Phe	His	Glu	Tyr	Leu	Asp	Ser	
			405					410					415			
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Met	Phe	Phe	Asp	Arg	Phe	Leu	Gln	Trp	Lys	Trp	Leu	Glu	Arg	Gln	Pro	
			420					425					430			
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Val	Thr	Lys	Asn	Thr	Phe	Arg	Gln	Tyr	Arg	Val	Leu	Gly	Lys	Gly	Gly	
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Phe	Gly	Glu	Val	Cys	Ala	Cys	Gln	Val	Arg	Ala	Thr	Gly	Lys	Met	Tyr	
	450					455					460					
gcc	tgc	aag	cgc	ttg	gag	aag	aag	agg	atc	aaa	aag	agg	aaa	ggg	gag	1440
Ala	Cys	Lys	Arg	Leu	Glu	Lys	Lys	Arg	Ile	Lys	Lys	Arg	Lys	Gly	Glu	
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Ser	Met	Ala	Leu	Asn	Glu	Lys	Gln	Ile	Leu	Glu	Lys	Val	Asn	Ser	Gln	
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Phe	Val	Val	Asn	Leu	Ala	Tyr	Ala	Tyr	Glu	Thr	Lys	Asp	Ala	Leu	Cys	
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Leu	Val	Leu	Thr	Ile	Met	Asn	Gly	Asp	Leu	Lys	Phe	His	Ile	Tyr		
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aac	atg	ggc	aac	cct	ggc	ttc	gag	gag	gag	cgg	gcc	ttg	ttt	tat	gcg	1632
Asn	Met	Gly	Asn	Pro	Gly	Phe	Glu	Glu	Glu	Arg	Ala	Leu	Phe	Tyr	Ala	
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gca	gag	atc	ctc	tgc	ggc	tta	gaa	gac	ctc	cac	cgt	gag	aac	acc	gtc	1680
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Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Ile	Leu	Leu	Asp	Asp	Tyr	Gly	His	
			565					570						575		
att	agg	atc	tca	gac	ctg	ggc	ttg	gct	gtg	aag	atc	ccc	gag	gga	gac	1776
Ile	Arg	Ile	Ser	Asp	Leu	Gly	Leu	Ala	Val	Lys	Ile	Pro	Glu	Gly	Asp	
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ctg	atc	cgc	ggc	cgg	gtg	ggc	act	gtt	ggc	tac	atg	gcc	ccc	gaa	gtc	1824
Leu	Ile	Arg	Gly	Arg	Val	Gly	Thr	Val	Gly	Tyr	Met	Ala	Pro	Glu	Val	
	595				600							605				
ctg	aac	aac	cag	agg	tac	ggc	ctg	agc	ccc	gac	tac	tggt	ggc	ctt	ggc	1872
Leu	Asn	Asn	Gln	Arg	Tyr	Gly	Leu	Ser	Pro	Asp	Tyr	Trp	Gly	Leu	Gly	

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Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro Phe Arg Gly Arg			
625	630	635	640
aag gag aag gtg aag cgg gag gag gtg gac cgc cgg gtc ctg gag acg			1968
Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg Val Leu Glu Thr			
645	650	655	
gag gag gtg tac tcc cac aag ttc tcc gag gag gcc aag tcc atc tgc			2016
Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala Lys Ser Ile Cys			
660	665	670	
aag atg ctg ctc acg aaa gat gcg aag cag agg ctg ggc tgc cag gag			2064
Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu Gly Cys Gln Glu			
675	680	685	
gag ggg gct gca gag gtc aag aga cac ccc ttc ttc agg aac atg aac			2112
Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe Arg Asn Met Asn			
690	695	700	
ttc aag cgc tta gaa gcc ggg atg ttg gac cct ccc ttc gtt cca gac			2160
Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro Phe Val Pro Asp			
705	710	715	720
ccc cgc gct gtg tac tgt aag gac gtg ctg gac atc gag cag ttc tcc			2208
Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile Glu Gln Phe Ser			
725	730	735	
act gtg aag ggc gtc aat ctg gac cac aca gac gac gac ttc tac tcc			2256
Thr Val Lys Gly Val Asn Leu Asp His Thr Asp Asp Asp Phe Tyr Ser			
740	745	750	
aag ttc tcc acg ggc tct gtg tcc atc cca tgg caa aac gag atg ata			2304
Lys Phe Ser Thr Gly Ser Val Ser Ile Pro Trp Gln Asn Glu Met Ile			
755	760	765	
gaa aca gaa tgc ttt aag gag ctg aac gtg ttt gga cct aat ggt acc			2352
Glu Thr Glu Cys Phe Lys Glu Leu Asn Val Phe Gly Pro Asn Gly Thr			
770	775	780	
ctc ccg cca gat ctg aac aga aac cac cct ccg gaa ccg ccc aag aaa			2400
Leu Pro Pro Asp Leu Asn Arg Asn His Pro Pro Glu Pro Pro Lys Lys			
785	790	795	800
ggg ctg ctc cag aga ctc ttc aag cgg cag cat cag aac aat tcc aag			2448
Gly Leu Leu Gln Arg Leu Phe Lys Arg Gln His Gln Asn Asn Ser Lys			
805	810	815	
agt tcg ccc agc tcc aag acc agt ttt aac cac cac ata aac tca aac			2496
Ser Ser Pro Ser Ser Lys Thr Ser Phe Asn His His Ile Asn Ser Asn			
820	825	830	
cat gtc agc tcg aac tcc acc gga agc agc tag			2529
His Val Ser Ser Asn Ser Thr Gly Ser Ser			
835	840		

<210> 43

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-Grk5 fusion

<400> 43

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
		35					40					45			
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70				75						80
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105					110		
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
145				150					155						160
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
			165					170						175	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
		180						185					190		
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
	195					200					205				
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
	210					215					220				
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
225					230				235						240
Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Ser	Met	Glu	Leu	Glu
			245					250					255		
Asn	Ile	Val	Ala	Asn	Thr	Val	Leu	Leu	Lys	Ala	Arg	Glu	Gly	Gly	Gly
		260					265						270		
Gly	Lys	Arg	Lys	Gly	Lys	Ser	Lys	Lys	Trp	Lys	Glu	Ile	Leu	Lys	Phe
	275						280					285			
Pro	His	Ile	Ser	Gln	Cys	Glu	Asp	Leu	Arg	Arg	Thr	Ile	Asp	Arg	Asp
	290					295					300				
Tyr	Cys	Ser	Leu	Cys	Asp	Lys	Gln	Pro	Ile	Gly	Arg	Leu	Leu	Phe	Arg
305					310				315						320
Gln	Phe	Cys	Glu	Thr	Arg	Pro	Gly	Leu	Glu	Cys	Tyr	Ile	Gln	Phe	Leu
			325						330					335	
Asp	Ser	Val	Ala	Glu	Tyr	Glu	Val	Thr	Pro	Asp	Glu	Lys	Leu	Gly	Glu
		340						345					350		
Lys	Gly	Lys	Glu	Ile	Met	Thr	Lys	Tyr	Leu	Thr	Pro	Lys	Ser	Pro	Val
	355						360					365			
Phe	Ile	Ala	Gln	Val	Gly	Gln	Asp	Leu	Val	Ser	Gln	Thr	Glu	Glu	Lys
	370					375					380				
Leu	Leu	Gln	Lys	Pro	Cys	Lys	Glu	Leu	Phe	Ser	Ala	Cys	Ala	Gln	Ser
385					390				395						400
Val	His	Glu	Tyr	Leu	Arg	Gly	Glu	Pro	Phe	His	Glu	Tyr	Leu	Asp	Ser
			405						410					415	
Met	Phe	Phe	Asp	Arg	Phe	Leu	Gln	Trp	Lys	Trp	Leu	Glu	Arg	Gln	Pro
		420						425					430		
Val	Thr	Lys	Asn	Thr	Phe	Arg	Gln	Tyr	Arg	Val	Leu	Gly	Lys	Gly	Gly
	435						440					445			
Phe	Gly	Glu	Val	Cys	Ala	Cys	Gln	Val	Arg	Ala	Thr	Gly	Lys	Met	Tyr
	450					455					460				
Ala	Cys	Lys	Arg	Leu	Glu	Lys	Lys	Arg	Ile	Lys	Lys	Arg	Lys	Gly	Glu
465					470				475						480
Ser	Met	Ala	Leu	Asn	Glu	Lys	Gln	Ile	Leu	Glu	Lys	Val	Asn	Ser	Gln
			485						490					495	
Phe	Val	Val	Asn	Leu	Ala	Tyr	Ala	Tyr	Glu	Thr	Lys	Asp	Ala	Leu	Cys
			500					505					510		

Leu	Val	Leu	Thr	Ile	Met	Asn	Gly	Gly	Asp	Leu	Lys	Phe	His	Ile	Tyr
	515						520					525			
Asn	Met	Gly	Asn	Pro	Gly	Phe	Glu	Glu	Glu	Arg	Ala	Leu	Phe	Tyr	Ala
	530					535					540				
Ala	Glu	Ile	Leu	Cys	Gly	Leu	Glu	Asp	Leu	His	Arg	Glu	Asn	Thr	Val
545					550					555					560
Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Ile	Leu	Leu	Asp	Asp	Tyr	Gly	His
			565						570					575	
Ile	Arg	Ile	Ser	Asp	Leu	Gly	Leu	Ala	Val	Lys	Ile	Pro	Glu	Gly	Asp
			580					585					590		
Leu	Ile	Arg	Gly	Arg	Val	Gly	Thr	Val	Gly	Tyr	Met	Ala	Pro	Glu	Val
	595					600						605			
Leu	Asn	Asn	Gln	Arg	Tyr	Gly	Leu	Ser	Pro	Asp	Tyr	Trp	Gly	Leu	Gly
	610					615					620				
Cys	Leu	Ile	Tyr	Glu	Met	Ile	Glu	Gly	Gln	Ser	Pro	Phe	Arg	Gly	Arg
625					630					635					640
Lys	Glu	Lys	Val	Lys	Arg	Glu	Glu	Val	Asp	Arg	Arg	Val	Leu	Glu	Thr
			645						650					655	
Glu	Glu	Val	Tyr	Ser	His	Lys	Phe	Ser	Glu	Glu	Ala	Lys	Ser	Ile	Cys
			660					665					670		
Lys	Met	Leu	Thr	Lys	Asp	Ala	Lys	Gln	Arg	Leu	Gly	Cys	Gln	Glu	
	675					680					685				
Glu	Gly	Ala	Ala	Glu	Val	Lys	Arg	His	Pro	Phe	Phe	Arg	Asn	Met	Asn
	690					695				700					
Phe	Lys	Arg	Leu	Glu	Ala	Gly	Met	Leu	Asp	Pro	Pro	Phe	Val	Pro	Asp
705					710					715					720
Pro	Arg	Ala	Val	Tyr	Cys	Lys	Asp	Val	Leu	Asp	Ile	Glu	Gln	Phe	Ser
			725						730					735	
Thr	Val	Lys	Gly	Val	Asn	Leu	Asp	His	Thr	Asp	Asp	Asp	Phe	Tyr	Ser
			740					745					750		
Lys	Phe	Ser	Thr	Gly	Ser	Val	Ser	Ile	Pro	Trp	Gln	Asn	Glu	Met	Ile
	755					760					765				
Glu	Thr	Glu	Cys	Phe	Lys	Glu	Leu	Asn	Val	Phe	Gly	Pro	Asn	Gly	Thr
	770					775					780				
Leu	Pro	Pro	Asp	Leu	Asn	Arg	Asn	His	Pro	Pro	Glu	Pro	Pro	Lys	Lys
785					790					795					800
Gly	Leu	Leu	Gln	Arg	Leu	Phe	Lys	Arg	Gln	His	Gln	Asn	Asn	Ser	Lys
			805						810					815	
Ser	Ser	Pro	Ser	Ser	Lys	Thr	Ser	Phe	Asn	His	His	Ile	Asn	Ser	Asn
			820					825					830		
His	Val	Ser	Ser	Asn	Ser	Thr	Gly	Ser	Ser						
	835						840								

<210> 44

<211> 1902

<212> DNA

<213> Artificial Sequence

<220>

<223> EGFP-Jnk1 fusion

<220>

<221> CDS

<222> (1)..(1899)

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<400> 44
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1      5      10      15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20      25      30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35      40      45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50      55      60
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag      240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65      70      75      80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85      90      95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100      105      110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115      120      125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130      135      140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145      150      155      160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165      170      175
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc      576
Val Gln Leu Ala Asp His Tyr Gln Asn Thr Pro Ile Gly Asp Gly
180      185      190
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg      624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195      200      205
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc      672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210      215      220
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc      720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225      230      235      240
gga ctc aga tct cga gct cga gcc atc atg agc aga agc aag cgt gac      768
Gly Leu Arg Ser Arg Ala Arg Ala Ile Met Ser Arg Ser Lys Arg Asp
245      250      255
aac aat ttt tat agt gta gag att gga gat tct aca ttc aca gtc ctg      816
Asn Asn Phe Tyr Ser Val Glu Ile Gly Asp Ser Thr Phe Thr Val Leu
260      265      270
aaa cga tat cag aat tta aaa cct ata ggc tca gga gct caa gga ata      864
Lys Arg Tyr Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile
275      280      285
gta tgc gca gct tat gat gcc att ctt gaa aga aat gtt gca atc aag      912
Val Cys Ala Ala Tyr Asp Ala Ile Leu Glu Arg Asn Val Ala Ile Lys
290      295      300
aag cta agc cga cca ttt cag aat cag act cat gcc aag cgg gcc tac      960

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Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln	Thr	His	Ala	Lys	Arg	Ala	Tyr		
305					310					315					320		
aga	gag	cta	gtt	ctt	atg	aaa	tgt	gtt	aat	cac	aaa	aat	ata	att	ggc	1008	
Arg	Glu	Leu	Val	Leu	Met	Lys	Cys	Val	Asn	His	Lys	Asn	Ile	Ile	Gly		
				325					330					335			
ctt	ttg	aat	gtt	ttc	aca	cca	cag	aaa	tcc	cta	gaa	gaa	ttt	caa	gat	1056	
Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys	Ser	Leu	Glu	Glu	Phe	Gln	Asp		
			340					345					350				
gtt	tac	ata	gtc	atg	gag	ctc	atg	gat	gca	aat	ctt	tgc	caa	gtg	att	1104	
Val	Tyr	Ile	Val	Met	Glu	Leu	Met	Asp	Ala	Asn	Leu	Cys	Gln	Val	Ile		
	355						360					365					
cag	atg	gag	cta	gat	cat	gaa	aga	atg	tcc	tac	ctt	ctc	tat	cag	atg	1152	
Gln	Met	Glu	Leu	Asp	His	Glu	Arg	Met	Ser	Tyr	Leu	Leu	Tyr	Gln	Met		
	370					375					380						
ctg	tgt	gga	atc	aag	cac	ctt	cat	tct	gct	gga	att	att	cat	cgg	gac	1200	
Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser	Ala	Gly	Ile	Ile	His	Arg	Asp		
	385				390					395					400		
tta	aag	ccc	agt	aat	ata	gta	gta	aaa	tct	gat	tgc	act	ttg	aag	att	1248	
Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys	Ser	Asp	Cys	Thr	Leu	Lys	Ile		
			405					410					415				
ctt	gac	ttc	ggt	ctg	gcc	agg	act	gca	gga	acg	agt	ttt	atg	atg	acg	1296	
Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala	Gly	Thr	Ser	Phe	Met	Met	Thr		
		420						425					430				
cct	tat	gta	gtg	act	cgc	tac	tac	aga	gca	ccc	gag	gtc	atc	ctt	ggc	1344	
Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	Ala	Pro	Glu	Val	Ile	Leu	Gly		
	435					440					445						
atg	ggc	tac	aag	gaa	aac	gtg	gat	tta	tgg	tct	gtg	ggg	tgc	att	atg	1392	
Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Leu	Trp	Ser	Val	Gly	Cys	Ile	Met		
	450				455						460						
gga	gaa	atg	gtt	tgc	cac	aaa	atc	ctc	ttt	cca	gga	agg	gac	tat	att	1440	
Gly	Glu	Met	Val	Cys	His	Lys	Ile	Leu	Phe	Pro	Gly	Arg	Asp	Tyr	Ile		
	465			470					475					480			
gat	cag	tgg	aat	aaa	gtt	att	gaa	cag	ctt	gga	aca	cca	tgt	cct	gaa	1488	
Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	Leu	Gly	Thr	Pro	Cys	Pro	Glu		
			485					490						495			
ttc	atg	aag	aaa	ctg	caa	cca	aca	gta	agg	act	tac	gtt	gaa	aac	aga	1536	
Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	Arg	Thr	Tyr	Val	Glu	Asn	Arg		
		500						505					510				
cct	aaa	tat	gct	gga	tat	agc	ttt	gag	aaa	ctc	ttc	cct	gat	gtc	ctt	1584	
Pro	Lys	Tyr	Ala	Gly	Tyr	Ser	Phe	Glu	Lys	Leu	Phe	Pro	Asp	Val	Leu		
	515					520					525						
ttc	cca	gct	gac	tca	gaa	cac	aac	aaa	ctt	aaa	gcc	agt	cag	gca	agg	1632	
Phe	Pro	Ala	Asp	Ser	Glu	His	Asn	Lys	Leu	Lys	Ala	Ser	Gln	Ala	Arg		
	530				535						540						
gat	ttg	tta	tcc	aaa	atg	ctg	gta	ata	gat	gca	tct	aaa	agg	atc	tct	1680	
Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	Asp	Ala	Ser	Lys	Arg	Ile	Ser		
	545				550				555					560			
gta	gat	gaa	gct	ctc	caa	cac	ccg	tac	atc	aat	gtc	tgg	tat	gat	cct	1728	
Val	Asp	Glu	Ala	Leu	Gln	His	Pro	Tyr	Ile	Asn	Val	Trp	Tyr	Asp	Pro		
			565					570					575				
tct	gaa	gca	gaa	gct	cca	cca	cca	aag	atc	cct	gac	aag	cag	tta	gat	1776	
Ser	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Lys	Ile	Pro	Asp	Lys	Gln	Leu	Asp		
		580						585					590				
gaa	agg	gaa	cac	aca	ata	gaa	gag	tgg	aaa	gaa	ttg	ata	tat	aag	gaa	1824	
Glu	Arg	Glu	His	Thr	Ile	Glu	Glu	Trp	Lys	Glu	Leu	Ile	Tyr	Lys	Glu		
	595					600					605						
gtt	atg	gac	ttg	gag	gag	aga	acc	aag	aat	gga	gtt	ata	cgg	ggg	cag	1872	
Val	Met	Asp	Leu	Glu	Glu	Arg	Thr	Lys	Asn	Gly	Val	Ile	Arg	Gly	Gln		
	610				615						620						
ccc	tct	cct	tta	gca	cag	gtg	cag	cag	tga							1902	
Pro	Ser	Pro	Leu	Ala	Gln	Val	Gln	Gln									
	625				630												

<210> 45  
 <211> 633  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> EGFP-Jnk1 fusion

<400> 45

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35      40      45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50      55      60
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65      70      75      80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85      90      95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100     105     110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115     120     125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130     135     140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145     150     155     160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165     170     175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180     185     190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195     200     205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210     215     220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225     230     235     240
Gly Leu Arg Ser Arg Ala Arg Ala Ile Met Ser Arg Ser Lys Arg Asp
245     250     255
Asn Asn Phe Tyr Ser Val Glu Ile Gly Asp Ser Thr Phe Thr Val Leu
260     265     270
Lys Arg Tyr Gln Asn Leu Lys Pro Ile Gly Ser Gly Ala Gln Gly Ile
275     280     285
Val Cys Ala Ala Tyr Asp Ala Ile Leu Glu Arg Asn Val Ala Ile Lys
290     295     300
Lys Leu Ser Arg Pro Phe Gln Asn Gln Thr His Ala Lys Arg Ala Tyr
305     310     315     320
Arg Glu Leu Val Leu Met Lys Cys Val Asn His Lys Asn Ile Ile Gly
325     330     335
Leu Leu Asn Val Phe Thr Pro Gln Lys Ser Leu Glu Glu Phe Gln Asp
340     345     350
Val Tyr Ile Val Met Glu Leu Met Asp Ala Asn Leu Cys Gln Val Ile
355     360     365

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Gln Met Glu Leu Asp His Glu Arg Met Ser Tyr Leu Leu Tyr Gln Met  
 370 375 380  
 Leu Cys Gly Ile Lys His Leu His Ser Ala Gly Ile Ile His Arg Asp  
 385 390 395 400  
 Leu Lys Pro Ser Asn Ile Val Val Lys Ser Asp Cys Thr Leu Lys Ile  
 405 410 415  
 Leu Asp Phe Gly Leu Ala Arg Thr Ala Gly Thr Ser Phe Met Met Thr  
 420 425 430  
 Pro Tyr Val Val Thr Arg Tyr Tyr Arg Ala Pro Glu Val Ile Leu Gly  
 435 440 445  
 Met Gly Tyr Lys Glu Asn Val Asp Leu Trp Ser Val Gly Cys Ile Met  
 450 455 460  
 Gly Glu Met Val Cys His Lys Ile Leu Phe Pro Gly Arg Asp Tyr Ile  
 465 470 475 480  
 Asp Gln Trp Asn Lys Val Ile Glu Gln Leu Gly Thr Pro Cys Pro Glu  
 485 490 495  
 Phe Met Lys Lys Leu Gln Pro Thr Val Arg Thr Tyr Val Glu Asn Arg  
 500 505 510  
 Pro Lys Tyr Ala Gly Tyr Ser Phe Glu Lys Leu Phe Pro Asp Val Leu  
 515 520 525  
 Phe Pro Ala Asp Ser Glu His Asn Lys Leu Lys Ala Ser Gln Ala Arg  
 530 535 540  
 Asp Leu Leu Ser Lys Met Leu Val Ile Asp Ala Ser Lys Arg Ile Ser  
 545 550 555 560  
 Val Asp Glu Ala Leu Gln His Pro Tyr Ile Asn Val Trp Tyr Asp Pro  
 565 570 575  
 Ser Glu Ala Glu Ala Pro Pro Pro Lys Ile Pro Asp Lys Gln Leu Asp  
 580 585 590  
 Glu Arg Glu His Thr Ile Glu Glu Trp Lys Glu Leu Ile Tyr Lys Glu  
 595 600 605  
 Val Met Asp Leu Glu Glu Arg Thr Lys Asn Gly Val Ile Arg Gly Gln  
 610 615 620  
 Pro Ser Pro Leu Ala Gln Val Gln Gln  
 625 630

<210> 46

<211> 1824

<212> DNA

<213> Artificial Sequence

<220>

<223> EGFP-p38 fusion

<220>

<221> CDS

<222> (1)..(1821)

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 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96



Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
		35					40					45					
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
	50					55					60						
ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag		240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys		
65					70					75					80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
			85						90					95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
		100						105					110				
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
	115						120					125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145					150					155					160		
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc		528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
			165					170						175			
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc		576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
		180					185					190					
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg		624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu		
	195					200						205					
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc		672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe		
	210					215					220						
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc		720
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser		
225					230					235					240		
gga	ctc	aga	tct	cga	ggg	aaa	atg	tct	cag	gag	agg	ccc	acg	ttc	tac		768
Gly	Leu	Arg	Ser	Arg	Gly	Lys	Met	Ser	Gln	Glu	Arg	Pro	Thr	Phe	Tyr		
			245						250					255			
cgg	cag	gag	ctg	aac	aag	aca	atc	tgg	gag	gtg	ccc	gag	cgt	tac	cag		816
Arg	Gln	Glu	Leu	Asn	Lys	Thr	Ile	Trp	Glu	Val	Pro	Glu	Arg	Tyr	Gln		
		260						265					270				
aac	ctg	tct	cca	gtg	ggc	tct	ggc	gcc	tat	ggc	tct	gtg	tgt	gct	gct		864
Asn	Leu	Ser	Pro	Val	Gly	Ser	Gly	Ala	Tyr	Gly	Ser	Val	Cys	Ala	Ala		
	275					280						285					
ttt	gac	aca	aaa	acg	ggg	tta	cgt	gtg	gca	gtg	aag	aag	ctc	tcc	aga		912
Phe	Asp	Thr	Lys	Thr	Gly	Leu	Arg	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg		
	290					295					300						
cca	ttt	cag	tcc	atc	att	cat	gcg	aaa	aga	acc	tac	aga	gaa	ctg	cgg		960
Pro	Phe	Gln	Ser	Ile	Ile	His	Ala	Lys	Arg	Thr	Tyr	Arg	Glu	Leu	Arg		
305					310					315					320		
tta	ctt	aaa	cat	atg	aaa	cat	gaa	aat	gtg	att	ggt	ctg	ttg	gac	gtt		1008
Leu	Leu	Lys	His	Met	Lys	His	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val		
			325					330						335			
ttt	aca	cct	gca	agg	tct	ctg	gag	gaa	ttc	aat	gat	gtg	tat	ctg	gtg		1056
Phe	Thr	Pro	Ala	Arg	Ser	Leu	Glu	Glu	Phe	Asn	Asp	Val	Tyr	Leu	Val		
		340						345					350				
acc	cat	ctc	atg	ggg	gca	gat	ctg	aac	aac	att	gtg	aaa	tgt	cag	aag		1104

Thr	His	Leu	Met	Gly	Ala	Asp	Leu	Asn	Asn	Ile	Val	Lys	Cys	Gln	Lys		
		355					360					365					
ctt	aca	gat	gac	cat	gtt	cag	ttc	ctt	atc	tac	caa	att	ctc	cga	ggt	1152	
Leu	Thr	Asp	Asp	His	Val	Gln	Phe	Leu	Ile	Tyr	Gln	Ile	Leu	Arg	Gly		
		370					375					380					
cta	aag	tat	ata	cat	tca	gct	gac	ata	att	cac	agg	gac	cta	aaa	cct	1200	
Leu	Lys	Tyr	Ile	His	Ser	Ala	Asp	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro		
					390					395					400		
agt	aat	cta	gct	gtg	aat	gaa	gac	tgt	gag	ctg	aag	att	ctg	gat	ttt	1248	
Ser	Asn	Leu	Ala	Val	Asn	Glu	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe		
				405					410						415		
gga	ctg	gct	cgg	cac	aca	gat	gat	gaa	atg	aca	ggc	tac	gtg	gcc	act	1296	
Gly	Leu	Ala	Arg	His	Thr	Asp	Asp	Glu	Met	Thr	Gly	Tyr	Val	Ala	Thr		
			420					425					430				
agg	tgg	tac	agg	gct	cct	gag	atc	atg	ctg	aac	tgg	atg	cat	tac	aac	1344	
Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Met	Leu	Asn	Trp	Met	His	Tyr	Asn		
		435					440						445				
cag	aca	gtt	gat	att	tgg	tca	gtg	gga	tgc	ata	atg	gcc	gag	ctg	ttg	1392	
Gln	Thr	Val	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Met	Ala	Glu	Leu	Leu		
		450				455					460						
act	gga	aga	aca	ttg	ttt	cct	ggt	aca	gac	cat	att	gat	cag	ttg	aag	1440	
Thr	Gly	Arg	Thr	Leu	Phe	Pro	Gly	Thr	Asp	His	Ile	Asp	Gln	Leu	Lys		
					470					475					480		
ctc	att	tta	aga	ctc	gtt	gga	acc	cca	ggg	gct	gag	ctt	ttg	aag	aaa	1488	
Leu	Ile	Leu	Arg	Leu	Val	Gly	Thr	Pro	Gly	Ala	Glu	Leu	Leu	Lys	Lys		
				485					490					495			
atc	tcc	tca	gag	tct	gca	aga	aac	tat	att	cag	tct	ttg	act	cag	atg	1536	
Ile	Ser	Ser	Glu	Ser	Ala	Arg	Asn	Tyr	Ile	Gln	Ser	Leu	Thr	Gln	Met		
			500					505					510				
ccg	aag	atg	aac	ttt	gcg	aat	gta	ttt	att	ggt	gcc	aat	ccc	ctg	gct	1584	
Pro	Lys	Met	Asn	Phe	Ala	Asn	Val	Phe	Ile	Gly	Ala	Asn	Pro	Leu	Ala		
		515					520					525					
gtc	gac	ttg	ctg	gag	aag	atg	ctt	gta	ttg	gac	tca	gat	aag	aga	att	1632	
Val	Asp	Leu	Leu	Glu	Lys	Met	Leu	Val	Leu	Asp	Ser	Asp	Lys	Arg	Ile		
		530				535						540					
aca	gcg	gcc	caa	gcc	ctt	gca	cat	gcc	tac	ttt	gct	cag	tac	cac	gat	1680	
Thr	Ala	Ala	Gln	Ala	Leu	Ala	His	Ala	Tyr	Phe	Ala	Gln	Tyr	His	Asp		
					550					555					560		
cct	gat	gat	gaa	cca	gtg	gcc	gat	cct	tat	gat	cag	tcc	ttt	gaa	agc	1728	
Pro	Asp	Asp	Glu	Pro	Val	Ala	Asp	Pro	Tyr	Asp	Gln	Ser	Phe	Glu	Ser		
				565					570					575			
agg	gac	ctc	ctt	ata	gat	gag	tgg	aaa	agc	ctg	acc	tat	gat	gaa	gtc	1776	
Arg	Asp	Leu	Leu	Ile	Asp	Glu	Trp	Lys	Ser	Leu	Thr	Tyr	Asp	Glu	Val		
			580					585					590				
atc	agc	ttt	gtg	cca	cca	ccc	ctt	gac	caa	gaa	gag	atg	gag	tcc	tga	1824	
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<210> 47

<211> 607

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-p38 fusion

<400> 47

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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
		35					40					45			
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70					75				80	
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105					110		
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
145					150					155				160	
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
				165					170					175	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
			180					185					190		
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
		195				200						205			
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
	210					215					220				
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
225					230					235				240	
Gly	Leu	Arg	Ser	Arg	Gly	Lys	Met	Ser	Gln	Glu	Arg	Pro	Thr	Phe	Tyr
			245						250					255	
Arg	Gln	Glu	Leu	Asn	Lys	Thr	Ile	Trp	Glu	Val	Pro	Glu	Arg	Tyr	Gln
			260					265					270		
Asn	Leu	Ser	Pro	Val	Gly	Ser	Gly	Ala	Tyr	Gly	Ser	Val	Cys	Ala	Ala
		275					280					285			
Phe	Asp	Thr	Lys	Thr	Gly	Leu	Arg	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg
	290				295						300				
Pro	Phe	Gln	Ser	Ile	Ile	His	Ala	Lys	Arg	Thr	Tyr	Arg	Glu	Leu	Arg
305					310					315				320	
Leu	Leu	Lys	His	Met	Lys	His	Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val
				325					330					335	
Phe	Thr	Pro	Ala	Arg	Ser	Leu	Glu	Glu	Phe	Asn	Asp	Val	Tyr	Leu	Val
			340					345					350		
Thr	His	Leu	Met	Gly	Ala	Asp	Leu	Asn	Asn	Ile	Val	Lys	Cys	Gln	Lys
		355					360					365			
Leu	Thr	Asp	Asp	His	Val	Gln	Phe	Leu	Ile	Tyr	Gln	Ile	Leu	Arg	Gly
	370					375					380				
Leu	Lys	Tyr	Ile	His	Ser	Ala	Asp	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro
385					390					395				400	
Ser	Asn	Leu	Ala	Val	Asn	Glu	Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe
			405						410					415	
Gly	Leu	Ala	Arg	His	Thr	Asp	Asp	Glu	Met	Thr	Gly	Tyr	Val	Ala	Thr
			420					425					430		
Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Met	Leu	Asn	Trp	Met	His	Tyr	Asn
		435					440					445			
Gln	Thr	Val	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Met	Ala	Glu	Leu	Leu
	450					455					460				
Thr	Gly	Arg	Thr	Leu	Phe	Pro	Gly	Thr	Asp	His	Ile	Asp	Gln	Leu	Lys
465					470					475				480	

Leu	Ile	Leu	Arg	Leu	Val	Gly	Thr	Pro	Gly	Ala	Glu	Leu	Leu	Lys	Lys
				485					490					495	
Ile	Ser	Ser	Glu	Ser	Ala	Arg	Asn	Tyr	Ile	Gln	Ser	Leu	Thr	Gln	Met
			500					505					510		
Pro	Lys	Met	Asn	Phe	Ala	Asn	Val	Phe	Ile	Gly	Ala	Asn	Pro	Leu	Ala
		515					520					525			
Val	Asp	Leu	Leu	Glu	Lys	Met	Leu	Val	Leu	Asp	Ser	Asp	Lys	Arg	Ile
	530					535					540				
Thr	Ala	Ala	Gln	Ala	Leu	Ala	His	Ala	Tyr	Phe	Ala	Gln	Tyr	His	Asp
545					550					555					560
Pro	Asp	Asp	Glu	Pro	Val	Ala	Asp	Pro	Tyr	Asp	Gln	Ser	Phe	Glu	Ser
			565						570					575	
Arg	Asp	Leu	Leu	Ile	Asp	Glu	Trp	Lys	Ser	Leu	Thr	Tyr	Asp	Glu	Val
		580						585					590		
Ile	Ser	Phe	Val	Pro	Pro	Pro	Leu	Asp	Gln	Glu	Glu	Met	Glu	Ser	
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<210> 48

<211> 2907

<212> DNA

<213> Artificial Sequence

<220>

<223> EGFP-p85alpha fusion

<220>

<221> CDS

<222> (1)..(2904)

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1				5					10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50				55				60							
ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
65				70				75					80			
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90					95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115					120					125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
		130				135					140						
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
		145			150					155					160		
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc		528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
			165					170						175			
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc		576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
		180					185						190				
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	ggc	ctg		624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu		
		195				200					205						
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc		672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe		
		210				215				220							
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc		720
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser		
				230						235					240		
gga	ctc	aga	tct	atg	agt	gct	gag	ggg	tac	cag	tac	aga	gcg	ctg	tat		768
Gly	Leu	Arg	Ser	Met	Ser	Ala	Glu	Gly	Tyr	Gln	Tyr	Arg	Ala	Leu	Tyr		
			245					250						255			
gat	tat	aaa	aag	gaa	aga	gaa	gaa	gat	att	gac	ttg	cac	ttg	ggc	gac		816
Asp	Tyr	Lys	Lys	Glu	Arg	Glu	Glu	Asp	Ile	Asp	Leu	His	Leu	Gly	Asp		
		260						265					270				
ata	ttg	act	gtg	aat	aaa	ggg	tcc	tta	gta	gct	ctt	gga	ttc	agt	gat		864
Ile	Leu	Thr	Val	Asn	Lys	Gly	Ser	Leu	Val	Ala	Leu	Gly	Phe	Ser	Asp		
		275				280						285					
gga	cag	gaa	gcc	agg	cct	gaa	gaa	att	ggc	tgg	tta	aat	ggc	tat	aat		912
Gly	Gln	Glu	Ala	Arg	Pro	Glu	Glu	Ile	Gly	Trp	Leu	Asn	Gly	Tyr	Asn		
		290			295					300							
gaa	acc	aca	ggg	gaa	agg	ggg	gac	ttt	ccg	gga	act	tac	gta	gaa	tat		960
Glu	Thr	Thr	Gly	Glu	Arg	Gly	Asp	Phe	Pro	Gly	Thr	Tyr	Val	Glu	Tyr		
			305			310				315					320		
att	gga	agg	aaa	aaa	atc	tcg	cct	ccc	aca	cca	aag	ccc	cgg	cca	cct		1008
Ile	Gly	Arg	Lys	Lys	Ile	Ser	Pro	Pro	Thr	Pro	Lys	Pro	Arg	Pro	Pro		
			325					330						335			
cgg	cct	ctt	cct	gtt	gca	cca	ggc	tct	tcg	aaa	act	gaa	gca	gat	gtt		1056
Arg	Pro	Leu	Pro	Val	Ala	Pro	Gly	Ser	Ser	Lys	Thr	Glu	Ala	Asp	Val		
			340					345						350			
gaa	caa	caa	gct	ttg	act	ctc	ccg	gat	ctt	gca	gag	cag	ttt	ggc	cct		1104
Glu	Gln	Gln	Ala	Leu	Thr	Leu	Pro	Asp	Leu	Ala	Glu	Gln	Phe	Ala	Pro		
		355					360					365					
cct	gac	att	gcc	ccg	cct	ctt	ctt	atc	aag	ctc	gtg	gaa	gcc	att	gaa		1152
Pro	Asp	Ile	Ala	Pro	Pro	Leu	Leu	Ile	Lys	Leu	Val	Glu	Ala	Ile	Glu		
		370				375					380						
aag	aaa	ggt	ctg	gaa	tgt	tca	act	cta	tac	aga	aca	cag	agc	tcc	agc		1200
Lys	Lys	Gly	Leu	Glu	Cys	Ser	Thr	Leu	Tyr	Arg	Thr	Gln	Ser	Ser	Ser		
		385			390					395					400		
aac	ctg	gca	gaa	tta	cga	cag	ctt	ctt	gat	tgt	gat	aca	ccc	tcc	gtg		1248
Asn	Leu	Ala	Glu	Leu	Arg	Gln	Leu	Leu	Asp	Cys	Asp	Thr	Pro	Ser	Val		
			405					410						415			
gac	ttg	gaa	atg	atc	gat	gtg	cac	gtt	ttg	gct	gac	gct	ttc	aaa	cgc		1296
Asp	Leu	Glu	Met	Ile	Asp	Val	His	Val	Leu	Ala	Asp	Ala	Phe	Lys	Arg		
		420						425					430				
tat	ctc	ctg	gac	tta	cca	aat	cct	gtc	att	cca	gca	gcc	gtt	tac	agt		1344
Tyr	Leu	Leu	Asp	Leu	Pro	Asn	Pro	Val	Ile	Pro	Ala	Ala	Val	Tyr	Ser		
		435				440						445					
gaa	atg	att	tct	tta	gct	cca	gaa	gta	caa	agc	tcc	gaa	gaa	tat	att		1392

Glu Met Ile Ser Leu Ala Pro Glu Val Gln Ser Ser Glu Glu Tyr Ile	
450 455 460	
cag cta ttg aag aag ctt att agg tgc cct agc ata cct cat cag tat	1440
Gln Leu Leu Lys Lys Leu Ile Arg Ser Pro Ser Ile Pro His Gln Tyr	
465 470 475 480	
tggttt acg ctt cag tat ttgtta aaa cat ttc ttc aag ctc tct caa	1488
Trp Leu Thr Leu Gln Tyr Leu Leu Lys His Phe Phe Lys Leu Ser Gln	
485 490 495	
acc tcc agc aaa aat ctgttg aat gca aga gta ctc tct gaa att ttc	1536
Thr Ser Ser Lys Asn Leu Leu Asn Ala Arg Val Leu Ser Glu Ile Phe	
500 505 510	
agc cct atg ctt ttc aga ttc tca gca gcc agc tct gat aat act gaa	1584
Ser Pro Met Leu Phe Arg Phe Ser Ala Ala Ser Ser Asp Asn Thr Glu	
515 520 525	
aac ctc ata aaa gtt ata gaa att tta atc tca act gaa tgg aat gaa	1632
Asn Leu Ile Lys Val Ile Glu Ile Leu Ile Ser Thr Glu Trp Asn Glu	
530 535 540	
cga cag cct gca cca gca ctg cct cct aaa cca cca aaa cct act act	1680
Arg Gln Pro Ala Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr	
545 550 555 560	
gta gcc aac aac ggt atg aat aac aat atg tcc tta caa aat gct gaa	1728
Val Ala Asn Asn Gly Met Asn Asn Asn Met Ser Leu Gln Asn Ala Glu	
565 570 575	
tggtac tgg gga gat atc tgc agg gaa gaa gtg aat gaa aaa ctt cga	1776
Trp Tyr Trp Gly Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg	
580 585 590	
gat aca gca gac ggg acc ttt ttgtga cga gat gcgtct act aaa atg	1824
Asp Thr Ala Asp Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met	
595 600 605	
cat ggt gat tat act ctt aca cta agg aaa ggg gga aat aac aaa tta	1872
His Gly Asp Tyr Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu	
610 615 620	
atc aaa ata ttt cat cga gat ggg aaa tat ggc ttc tct gac cca tta	1920
Ile Lys Ile Phe His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu	
625 630 635 640	
acc ttc agt tct gtgtgtt gaa tta ata aac cac tac cgg aat gaa tct	1968
Thr Phe Ser Ser Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser	
645 650 655	
cta gct cag tat aat ccc aaa ttgtat gtg aaa tta ctt tat cca gta	2016
Leu Ala Gln Tyr Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val	
660 665 670	
tcc aaa tac caa cag gat caa gtt gtc aaa gaa gat aat att gaa gct	2064
Ser Lys Tyr Gln Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala	
675 680 685	
gta ggg aaa aaa tta cat gaa tat aac act cag ttt caa gaa aaa agt	2112
Val Gly Lys Lys Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser	
690 695 700	
cga gaa tat gat aga tta tat gaa gaa tat acc cgc aca tcc cag gaa	2160
Arg Glu Tyr Asp Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu	
705 710 715 720	
atc caa atg aaa agg aca gct att gaa gca ttt aat gaa acc ata aaa	2208
Ile Gln Met Lys Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys	
725 730 735	
ata ttt gaa gaa cag tgc cag acc caa gag cgg tac agc aaa gaa tac	2256
Ile Phe Glu Glu Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr	
740 745 750	
ata gaa aag ttt aaa cgt gaa ggc aat gag aaa gaa ata caa agg att	2304
Ile Glu Lys Phe Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile	
755 760 765	
atg cat aat tat gat aag ttgttg aag tct cga atc agt gaa att att gac	2352
Met His Asn Tyr Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp	
770 775 780	
agt aga aga aga ttgttg gaa gaa gac ttgttg aag aag cag gca gct gag tat	2400

Ser	Arg	Arg	Arg	Leu	Glu	Glu	Asp	Leu	Lys	Lys	Gln	Ala	Ala	Glu	Tyr	
785					790					795					800	
cga	gaa	att	gac	aaa	cgt	atg	aac	agc	att	aaa	cca	gac	ctt	atc	cag	2448
Arg	Glu	Ile	Asp	Lys	Arg	Met	Asn	Ser	Ile	Lys	Pro	Asp	Leu	Ile	Gln	
				805					810					815		
ctg	aga	aag	acg	aga	gac	caa	tac	ttg	atg	tgg	ttg	act	caa	aaa	ggg	2496
Leu	Arg	Lys	Thr	Arg	Asp	Gln	Tyr	Leu	Met	Trp	Leu	Thr	Gln	Lys	Gly	
				820					825					830		
ggt	cgg	caa	aag	aag	ttg	aac	gag	tgg	ttg	ggc	aat	gaa	aac	act	gaa	2544
Val	Arg	Gln	Lys	Lys	Leu	Asn	Glu	Trp	Leu	Gly	Asn	Glu	Asn	Thr	Glu	
				835					840					845		
gac	caa	tat	tca	ctg	gtg	gaa	gat	gat	gaa	gat	ttg	ccc	cat	cat	gat	2592
Asp	Gln	Tyr	Ser	Leu	Val	Glu	Asp	Asp	Glu	Asp	Leu	Pro	His	His	Asp	
				850										860		
gag	aag	aca	tgg	aat	gtt	gga	agc	agc	aac	cga	aac	aaa	gct	gaa	aac	2640
Glu	Lys	Thr	Trp	Asn	Val	Gly	Ser	Ser	Asn	Arg	Asn	Lys	Ala	Glu	Asn	
					870										880	
ctg	ttg	cga	ggg	aag	cga	gat	ggc	act	ttt	ctt	gtc	cgg	gag	agc	agt	2688
Leu	Leu	Arg	Gly	Lys	Arg	Asp	Gly	Thr	Phe	Leu	Val	Arg	Glu	Ser	Ser	
				885										895		
aaa	cag	ggc	tgc	tat	gcc	tgc	tct	gta	gtg	gtg	gac	ggc	gaa	gta	aag	2736
Lys	Gln	Gly	Cys	Tyr	Ala	Cys	Ser	Val	Val	Val	Asp	Gly	Glu	Val	Lys	
				900										910		
cat	tgt	gtc	ata	aac	aaa	aca	gca	act	ggc	tat	ggc	ttt	gcc	gag	ccc	2784
His	Cys	Val	Ile	Asn	Lys	Thr	Ala	Thr	Gly	Tyr	Gly	Phe	Ala	Glu	Pro	
				915										925		
tat	aac	ttg	tac	agc	tct	ctg	aaa	gaa	ctg	gtg	cta	cat	tac	caa	cac	2832
Tyr	Asn	Leu	Tyr	Ser	Ser	Leu	Lys	Glu	Leu	Val	Leu	His	Tyr	Gln	His	
						935								940		
acc	tcc	ctt	gtg	cag	cac	aac	gac	tcc	ctc	aat	gtc	aca	cta	gcc	tac	2880
Thr	Ser	Leu	Val	Gln	His	Asn	Asp	Ser	Leu	Asn	Val	Thr	Leu	Ala	Tyr	
					950										960	
cca	gta	tat	gca	cag	cag	agg	cga	tga								2907
Pro	Val	Tyr	Ala	Gln	Gln	Arg	Arg									
					965											

<210> 49

<211> 968

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-p85alpha fusion

<400> 49

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			20					25					30			
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40						45			
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70					75					80	

Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105					110		
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn
	145				150					155					160
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser
			165					170						175	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly
			180					185					190		
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu
	195					200						205			
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
	210					215					220				
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
	225					230				235					240
Gly	Leu	Arg	Ser	Met	Ser	Ala	Glu	Gly	Tyr	Gln	Tyr	Arg	Ala	Leu	Tyr
			245						250					255	
Asp	Tyr	Lys	Lys	Glu	Arg	Glu	Glu	Asp	Ile	Asp	Leu	His	Leu	Gly	Asp
			260					265					270		
Ile	Leu	Thr	Val	Asn	Lys	Gly	Ser	Leu	Val	Ala	Leu	Gly	Phe	Ser	Asp
	275						280						285		
Gly	Gln	Glu	Ala	Arg	Pro	Glu	Glu	Ile	Gly	Trp	Leu	Asn	Gly	Tyr	Asn
	290					295						300			
Glu	Thr	Thr	Gly	Glu	Arg	Gly	Asp	Phe	Pro	Gly	Thr	Tyr	Val	Glu	Tyr
	305					310				315					320
Ile	Gly	Arg	Lys	Lys	Ile	Ser	Pro	Pro	Thr	Pro	Lys	Pro	Arg	Pro	Pro
			325						330					335	
Arg	Pro	Leu	Pro	Val	Ala	Pro	Gly	Ser	Ser	Lys	Thr	Glu	Ala	Asp	Val
			340					345					350		
Glu	Gln	Gln	Ala	Leu	Thr	Leu	Pro	Asp	Leu	Ala	Glu	Gln	Phe	Ala	Pro
			355				360					365			
Pro	Asp	Ile	Ala	Pro	Pro	Leu	Leu	Ile	Lys	Leu	Val	Glu	Ala	Ile	Glu
	370					375					380				
Lys	Lys	Gly	Leu	Glu	Cys	Ser	Thr	Leu	Tyr	Arg	Thr	Gln	Ser	Ser	Ser
	385				390					395					400
Asn	Leu	Ala	Glu	Leu	Arg	Gln	Leu	Leu	Asp	Cys	Asp	Thr	Pro	Ser	Val
			405						410					415	
Asp	Leu	Glu	Met	Ile	Asp	Val	His	Val	Leu	Ala	Asp	Ala	Phe	Lys	Arg
			420					425					430		
Tyr	Leu	Leu	Asp	Leu	Pro	Asn	Pro	Val	Ile	Pro	Ala	Ala	Val	Tyr	Ser
	435					440						445			
Glu	Met	Ile	Ser	Leu	Ala	Pro	Glu	Val	Gln	Ser	Ser	Glu	Glu	Tyr	Ile
	450					455					460				
Gln	Leu	Leu	Lys	Lys	Leu	Ile	Arg	Ser	Pro	Ser	Ile	Pro	His	Gln	Tyr
	465				470					475					480
Trp	Leu	Thr	Leu	Gln	Tyr	Leu	Leu	Lys	His	Phe	Phe	Lys	Leu	Ser	Gln
			485						490					495	
Thr	Ser	Ser	Lys	Asn	Leu	Leu	Asn	Ala	Arg	Val	Leu	Ser	Glu	Ile	Phe
			500					505					510		
Ser	Pro	Met	Leu	Phe	Arg	Phe	Ser	Ala	Ala	Ser	Ser	Asp	Asn	Thr	Glu
		515					520					525			
Asn	Leu	Ile	Lys	Val	Ile	Glu	Ile	Leu	Ile	Ser	Thr	Glu	Trp	Asn	Glu
	530					535					540				
Arg	Gln	Pro	Ala	Pro	Ala	Leu	Pro	Pro	Lys	Pro	Pro	Lys	Pro	Thr	Thr
	545				550					555					560
Val	Ala	Asn	Asn	Gly	Met	Asn	Asn	Asn	Met	Ser	Leu	Gln	Asn	Ala	Glu
			565						570					575	
Trp	Tyr	Trp	Gly	Asp	Ile	Ser	Arg	Glu	Glu	Val	Asn	Glu	Lys	Leu	Arg





<223> EGFP-Smad2 fusion

<220>

<221> CDS

<222> (1)..(2157)

<400> 50

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Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1			5						10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40						45			
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70				75					80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130				135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145				150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
			165					170						175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
			180					185					190			
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195				200					205				
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
	210					215					220					
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc	720
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225				230					235				240		
gga	ctc	aga	tct	cga	gct	caa	gct	tcg	aat	tcg	acc	atg	tcg	tcc	atc	768
Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Thr	Met	Ser	Ser	Ile	
			245					250						255		
ttg	cca	ttc	acg	ccg	cca	gtt	gtg	aag	aga	ctg	ctg	gga	tgg	aag	aag	816
Leu	Pro	Phe	Thr	Pro	Pro	Val	Val	Lys	Arg	Leu	Leu	Gly	Trp	Lys	Lys	
			260					265					270			
tca	gct	ggt	ggg	tct	gga	gga	gca	ggc	gga	gga	gag	cag	aat	ggg	cag	864

Ser	Ala	Gly	Gly	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Glu	Gln	Asn	Gly	Gln		
		275					280					285					
gaa	gaa	aag	tgg	tgt	gag	aaa	gca	gtg	aaa	agt	ctg	gtg	aag	aag	cta	912	
Glu	Glu	Lys	Trp	Cys	Glu	Lys	Ala	Val	Lys	Ser	Leu	Val	Lys	Lys	Leu		
		290					295				300						
aag	aaa	aca	gga	cga	tta	gat	gag	ctt	gag	aaa	gcc	atc	acc	act	caa	960	
Lys	Lys	Thr	Gly	Arg	Leu	Asp	Glu	Leu	Glu	Lys	Ala	Ile	Thr	Thr	Gln		
		305				310				315					320		
aac	tgt	aat	act	aaa	tgt	gtt	acc	ata	cca	agc	act	tgc	tct	gaa	att	1008	
Asn	Cys	Asn	Thr	Lys	Cys	Val	Thr	Ile	Pro	Ser	Thr	Cys	Ser	Glu	Ile		
				325					330					335			
tgg	gga	ctg	agt	aca	cca	aat	acg	ata	gat	cag	tgg	gat	aca	aca	ggc	1056	
Trp	Gly	Leu	Ser	Thr	Pro	Asn	Thr	Ile	Asp	Gln	Trp	Asp	Thr	Thr	Gly		
				340					345					350			
ctt	tac	agc	ttc	tct	gaa	caa	acc	agg	tct	ctt	gat	ggt	cgt	ctc	cag	1104	
Leu	Tyr	Ser	Phe	Ser	Glu	Gln	Thr	Arg	Ser	Leu	Asp	Gly	Arg	Leu	Gln		
		355					360					365					
gta	tcc	cat	cga	aaa	gga	ttg	cca	cat	gtt	ata	tat	tgc	cga	tta	tgg	1152	
Val	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr	Cys	Arg	Leu	Trp		
		370				375						380					
cgc	tgg	cct	gat	ctt	cac	agt	cat	cat	gaa	ctc	aag	gca	att	gaa	aac	1200	
Arg	Trp	Pro	Asp	Leu	His	Ser	His	His	Glu	Leu	Lys	Ala	Ile	Glu	Asn		
					390				395					400			
tgc	gaa	tat	gct	ttt	aat	ctt	aaa	aag	gat	gaa	gta	tgt	gta	aac	cct	1248	
Cys	Glu	Tyr	Ala	Phe	Asn	Leu	Lys	Lys	Asp	Glu	Val	Cys	Val	Asn	Pro		
				405					410					415			
tac	cac	tat	cag	aga	gtt	gag	aca	cca	gtt	ttg	cct	cca	gta	tta	gtg	1296	
Tyr	His	Tyr	Gln	Arg	Val	Glu	Thr	Pro	Val	Leu	Pro	Pro	Val	Leu	Val		
				420				425						430			
ccc	cga	cac	acc	gag	atc	cta	aca	gaa	ctt	ccg	cct	ctg	gat	gac	tat	1344	
Pro	Arg	His	Thr	Glu	Ile	Leu	Thr	Glu	Leu	Pro	Pro	Leu	Asp	Asp	Tyr		
				435			440					445					
act	cac	tcc	att	cca	gaa	aac	act	aac	ttc	cca	gca	gga	att	gag	cca	1392	
Thr	His	Ser	Ile	Pro	Glu	Asn	Thr	Asn	Phe	Pro	Ala	Gly	Ile	Glu	Pro		
				450		455					460						
cag	agt	aat	tat	att	cca	gaa	acg	cca	cct	cct	gga	tat	atc	agt	gaa	1440	
Gln	Ser	Asn	Tyr	Ile	Pro	Glu	Thr	Pro	Pro	Pro	Gly	Tyr	Ile	Ser	Glu		
				465		470				475				480			
gat	gga	gaa	aca	agt	gac	caa	cag	ttg	aat	caa	agt	atg	gac	aca	ggc	1488	
Asp	Gly	Glu	Thr	Ser	Asp	Gln	Gln	Leu	Asn	Gln	Ser	Met	Asp	Thr	Gly		
				485				490						495			
tct	cca	gca	gaa	cta	tct	cct	act	act	ctt	tcc	cct	gtt	aat	cat	agc	1536	
Ser	Pro	Ala	Glu	Leu	Ser	Pro	Thr	Thr	Leu	Ser	Pro	Val	Asn	His	Ser		
				500				505						510			
ttg	gat	tta	cag	cca	gtt	act	tac	tca	gaa	cct	gca	ttt	tgg	tgt	tca	1584	
Leu	Asp	Leu	Gln	Pro	Val	Thr	Tyr	Ser	Glu	Pro	Ala	Phe	Trp	Cys	Ser		
				515			520							525			
ata	gca	tat	tat	gaa	tta	aat	cag	agg	gtt	gga	gaa	acc	ttc	cat	gca	1632	
Ile	Ala	Tyr	Tyr	Glu	Leu	Asn	Gln	Arg	Val	Gly	Glu	Thr	Phe	His	Ala		
				530		535					540						
tca	cag	ccc	tca	ctc	act	gta	gat	ggc	ttt	aca	gac	cca	tca	aat	tca	1680	
Ser	Gln	Pro	Ser	Leu	Thr	Val	Asp	Gly	Phe	Thr	Asp	Pro	Ser	Asn	Ser		
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gag	agg	ttc	tgc	tta	ggt	tta	ctc	tcc	aat	gtt	aac	cga	aat	gcc	acg	1728	
Glu	Arg	Phe	Cys	Leu	Gly	Leu	Leu	Ser	Asn	Val	Asn	Arg	Asn	Ala	Thr		
				565				570						575			
gta	gaa	atg	aca	aga	agg	cat	ata	gga	aga	gga	gtg	cgc	tta	tac	tac	1776	
Val	Glu	Met	Thr	Arg	Arg	His	Ile	Gly	Arg	Gly	Val	Arg	Leu	Tyr	Tyr		
				580			585							590			
ata	ggt	ggg	gaa	gtt	ttt	gct	gag	tgc	cta	agt	gat	agt	gca	atc	ttt	1824	
Ile	Gly	Gly	Glu	Val	Phe	Ala	Glu	Cys	Leu	Ser	Asp	Ser	Ala	Ile	Phe		
				595		600						605					
gtg	cag	agc	ccc	aat	tgt	aat	cag	aga	tat	ggc	tgg	cac	cct	gca	aca	1872	

Val	Gln	Ser	Pro	Asn	Cys	Asn	Gln	Arg	Tyr	Gly	Trp	His	Pro	Ala	Thr		
610						615					620						
gtg	tgt	aaa	att	cca	cca	ggc	tgt	aat	ctg	aag	atc	ttc	aac	aac	cag	1920	
Val	Cys	Lys	Ile	Pro	Pro	Gly	Cys	Asn	Leu	Lys	Ile	Phe	Asn	Asn	Gln		
625						630				635					640		
gaa	ttt	gct	gct	ctt	ctg	gct	cag	tct	gtt	aat	cag	ggg	ttt	gaa	gcc	1968	
Glu	Phe	Ala	Ala	Leu	Leu	Ala	Gln	Ser	Val	Asn	Gln	Gly	Phe	Glu	Ala		
				645						650					655		
gtc	tat	cag	cta	act	aga	atg	tgc	acc	ata	aga	atg	agt	ttt	gtg	aaa	2016	
Val	Tyr	Gln	Leu	Thr	Arg	Met	Cys	Thr	Ile	Arg	Met	Ser	Phe	Val	Lys		
				660						665					670		
ggg	tgg	gga	gca	gaa	tac	cga	agg	cag	acg	gta	aca	agt	act	cct	tgc	2064	
Gly	Trp	Gly	Ala	Glu	Tyr	Arg	Arg	Gln	Thr	Val	Thr	Ser	Thr	Pro	Cys		
		675					680						685				
tgg	att	gaa	ctt	cat	ctg	aat	gga	cct	cta	cag	tgg	ttg	gac	aaa	gta	2112	
Trp	Ile	Glu	Leu	His	Leu	Asn	Gly	Pro	Leu	Gln	Trp	Leu	Asp	Lys	Val		
	690					695				700							
tta	act	cag	atg	gga	tcc	cct	tca	gtg	cgt	tgc	tca	agc	atg	tca	taa	2160	
Leu	Thr	Gln	Met	Gly	Ser	Pro	Ser	Val	Arg	Cys	Ser	Ser	Met	Ser			
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<210> 51

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-Smad2 fusion

<400> 51

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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
		35					40					45					
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
		50			55					60							
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys		
65				70					75					80			
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
			85					90					95				
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
			100				105						110				
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115				120						125					
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130				135					140							
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145				150					155					160			
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
			165				170						175				
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
		180					185					190					
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu		

	195		200		205
Ser	Lys	Asp	Pro	Asn	Glu
210					
Val	Thr	Ala	Ala	Gly	Ile
225					
Gly	Leu	Arg	Ser	Arg	Ala
Leu	Pro	Phe	Thr	Pro	Pro
Ser	Ala	Gly	Gly	Ser	Gly
Glu	Glu	Lys	Trp	Cys	Glu
290					
Lys	Lys	Thr	Gly	Arg	Leu
305					
Asn	Cys	Asn	Thr	Lys	Cys
Trp	Gly	Leu	Ser	Thr	Pro
Leu	Tyr	Ser	Phe	Ser	Glu
Val	Ser	His	Arg	Lys	Gly
370					
Arg	Trp	Pro	Asp	Leu	His
385					
Cys	Glu	Tyr	Ala	Phe	Asn
Tyr	His	Tyr	Gln	Arg	Val
Pro	Arg	His	Thr	Glu	Ile
Thr	His	Ser	Ile	Pro	Glu
450					
Gln	Ser	Asn	Tyr	Ile	Pro
465					
Asp	Gly	Glu	Thr	Ser	Asp
Ser	Pro	Ala	Glu	Leu	Ser
Leu	Asp	Leu	Gln	Pro	Val
Ile	Ala	Tyr	Tyr	Glu	Leu
530					
Ser	Gln	Pro	Ser	Leu	Thr
545					
Glu	Arg	Phe	Cys	Leu	Gly
Val	Glu	Met	Thr	Arg	Arg
Ile	Gly	Gly	Glu	Val	Phe
Val	Gln	Ser	Pro	Asn	Cys
610					
Val	Cys	Lys	Ile	Pro	Pro
625					
Glu	Phe	Ala	Ala	Leu	Leu
Val	Tyr	Gln	Leu	Thr	Arg
Gly	Trp	Gly	Ala	Glu	Tyr
Trp	Ile	Glu	Leu	His	Leu
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Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser Met Ser  
 705 710 715

<210> 52

<211> 2421

<212> DNA

<213> Artificial Sequence

<220>

<223> EGFP-Smad4 fusion

<220>

<221> CDS

<222> (1)..(2418)

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 1 5 10 15  
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96  
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
 20 25 30  
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
 35 40 45  
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190

ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
	195					200					205					
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
	210					215					220					
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc	720
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
	225				230					235					240	
gga	ctc	aga	tct	cga	gct	caa	gct	tcg	aat	tcg	aat	tca	acc	atg	gac	768
Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Asn	Ser	Thr	Met	Asp	
				245					250					255		
aat	atg	tct	att	acg	aat	aca	cca	aca	agt	aat	gat	gcc	tgt	ctg	agc	816
Asn	Met	Ser	Ile	Thr	Asn	Thr	Pro	Thr	Ser	Asn	Asp	Ala	Cys	Leu	Ser	
			260					265					270			
att	gtg	cat	agt	ttg	atg	tgc	cat	aga	caa	ggg	gga	gag	agt	gaa	aca	864
Ile	Val	His	Ser	Leu	Met	Cys	His	Arg	Gln	Gly	Gly	Glu	Ser	Glu	Thr	
	275					280						285				
ttt	gca	aaa	aga	gca	att	gaa	agt	ttg	gta	aag	aag	ctg	aag	gag	aaa	912
Phe	Ala	Lys	Arg	Ala	Ile	Glu	Ser	Leu	Val	Lys	Lys	Leu	Lys	Glu	Lys	
	290					295				300						
aaa	gat	gaa	ttg	gat	tct	tta	ata	aca	gct	ata	act	aca	aat	gga	gct	960
Lys	Asp	Glu	Leu	Asp	Ser	Leu	Ile	Thr	Ala	Ile	Thr	Thr	Asn	Gly	Ala	
	305				310				315					320		
cat	cct	agt	aaa	tgt	gtt	acc	ata	cag	aga	aca	ttg	gat	ggg	agg	ctt	1008
His	Pro	Ser	Lys	Cys	Val	Thr	Ile	Gln	Arg	Thr	Leu	Asp	Gly	Arg	Leu	
			325					330					335			
cag	gtg	gct	ggg	cgg	aaa	gga	ttt	cct	cat	gtg	atc	tat	gcc	cgt	ctc	1056
Gln	Val	Ala	Gly	Arg	Lys	Gly	Phe	Pro	His	Val	Ile	Tyr	Ala	Arg	Leu	
			340					345				350				
tgg	agg	tgg	cct	gat	ctt	cac	aaa	aat	gaa	cta	aaa	cat	gtt	aaa	tat	1104
Trp	Arg	Trp	Pro	Asp	Leu	His	Lys	Asn	Glu	Leu	Lys	His	Val	Lys	Tyr	
	355					360						365				
tgt	cag	tat	gcg	ttt	gac	tta	aaa	tgt	gat	agt	gtc	tgt	gtg	aat	cca	1152
Cys	Gln	Tyr	Ala	Phe	Asp	Leu	Lys	Cys	Asp	Ser	Val	Cys	Val	Asn	Pro	
	370				375						380					
tat	cac	tac	gaa	cga	gtt	gta	tca	cct	gga	att	gat	ctc	tca	gga	tta	1200
Tyr	His	Tyr	Glu	Arg	Val	Val	Ser	Pro	Gly	Ile	Asp	Leu	Ser	Gly	Leu	
	385				390					395				400		
aca	ctg	cag	agt	aat	gct	cca	tca	agt	atg	atg	gtg	aag	gat	gaa	tat	1248
Thr	Leu	Gln	Ser	Asn	Ala	Pro	Ser	Ser	Met	Met	Val	Lys	Asp	Glu	Tyr	
			405					410				415				
gtg	cat	gac	ttt	gag	gga	cag	cca	tcg	ttg	tcc	act	gaa	gga	cat	tca	1296
Val	His	Asp	Phe	Glu	Gly	Gln	Pro	Ser	Leu	Ser	Thr	Glu	Gly	His	Ser	
			420					425				430				
att	caa	acc	atc	cag	cat	cca	cca	agt	aat	cgt	gca	tcg	aca	gag	aca	1344
Ile	Gln	Thr	Ile	Gln	His	Pro	Pro	Ser	Asn	Arg	Ala	Ser	Thr	Glu	Thr	
	435					440					445					
tac	agc	acc	cca	gct	ctg	tta	gcc	cca	tct	gag	tct	aat	gct	acc	agc	1392
Tyr	Ser	Thr	Pro	Ala	Leu	Leu	Ala	Pro	Ser	Glu	Ser	Asn	Ala	Thr	Ser	
	450				455						460					
act	gcc	aac	ttt	ccc	aac	att	cct	gtg	gct	tcc	aca	agt	cag	cct	gcc	1440
Thr	Ala	Asn	Phe	Pro	Asn	Ile	Pro	Val	Ala	Ser	Thr	Ser	Gln	Pro	Ala	
	465				470					475				480		
agt	ata	ctg	ggg	ggc	agc	cat	agt	gaa	gga	ctg	ttg	cag	ata	gca	tca	1488
Ser	Ile	Leu	Gly	Gly	Ser	His	Ser	Glu	Gly	Leu	Leu	Gln	Ile	Ala	Ser	
			485					490				495				
ggg	cct	cag	cca	gga	cag	cag	cag	aat	gga	ttt	act	ggg	cag	cca	gct	1536
Gly	Pro	Gln	Pro	Gly	Gln	Gln	Gln	Asn	Gly	Phe	Thr	Gly	Gln	Pro	Ala	
			500					505				510				
act	tac	cat	cat	aac	agc	act	acc	acc	tgg	act	gga	agt	agg	act	gca	1584
Thr	Tyr	His	His	Asn	Ser	Thr	Thr	Thr	Trp	Thr	Gly	Ser	Arg	Thr	Ala	
	515						520					525				

cca tac aca cct aat ttg cct cac cac caa aac ggc cat ctt cag cac	1632
Pro Tyr Thr Pro Asn Leu Pro His His Gln Asn Gly His Leu Gln His	
530 535 540	
cac ccg cct atg ccg ccc cat ccc gga cat tac tgg cct gtt cac aat	1680
His Pro Pro Met Pro Pro His Pro Gly His Tyr Trp Pro Val His Asn	
545 550 555 560	
gag ctt gca ttc cag cct ccc att tcc aat cat cct gct cct gag tat	1728
Glu Leu Ala Phe Gln Pro Pro Ile Ser Asn His Pro Ala Pro Glu Tyr	
565 570 575	
tgg tgt tcc att gct tac ttt gaa atg gat gtt cag gta gga gag aca	1776
Trp Cys Ser Ile Ala Tyr Phe Glu Met Asp Val Gln Val Gly Glu Thr	
580 585 590	
ttt aag gtt cct tca agc tgc cct att gtt act gtt gat gga tac gtg	1824
Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly Tyr Val	
595 600 605	
gac cct tct gga gga gat cgc ttt tgt ttg ggt caa ctc tcc aat gtc	1872
Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser Asn Val	
610 615 620	
cac agg aca gaa gcc att gag aga gca agg ttg cac ata ggc aaa ggt	1920
His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly Lys Gly	
625 630 635 640	
gtg cag ttg gaa tgt aaa ggt gaa ggt gat gtt tgg gtc agg tgc ctt	1968
Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg Cys Leu	
645 650 655	
agt gac cac gcg gtc ttt gta cag agt tac tac tta gac aga gaa gct	2016
Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg Glu Ala	
660 665 670	
ggg cgt gca cct gga gat gct gtt cat aag atc tac cca agt gca tat	2064
Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser Ala Tyr	
675 680 685	
ata aag gtc ttt gat ttg cgt cag tgt cat cga cag atg cag cag cag	2112
Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln Gln Gln	
690 695 700	
gcg gct act gca caa gct gca gca gct gcc cag gca gca gcc gtg gca	2160
Ala Ala Thr Ala Gln Ala Ala Ala Ala Ala Gln Ala Ala Val Ala	
705 710 715 720	
gga aac atc cct ggc cca gga tca gta ggt gga ata gct cca gct atc	2208
Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro Ala Ile	
725 730 735	
agt ctg tca gct gct gct gga att ggt gtt gat gac ctt cgt cgc tta	2256
Ser Leu Ser Ala Ala Ala Gly Ile Gly Val Asp Asp Leu Arg Arg Leu	
740 745 750	
tgc ata ctc agg atg agt ttt gtg aaa ggc tgg gga ccg gat tac cca	2304
Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp Tyr Pro	
755 760 765	
aga cag agc atc aaa gaa aca cct tgc tgg att gaa att cac tta cac	2352
Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His Leu His	
770 775 780	
cgg gcc ctc cag ctc cta gac gaa gta ctt cat acc atg ccg att gca	2400
Arg Ala Leu Gln Leu Leu Asp Glu Val Leu His Thr Met Pro Ile Ala	
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gac cca caa cct tta gac tga	2421
Asp Pro Gln Pro Leu Asp	
805	

<210> 53

<211> 806

<212> PRT



<213> Artificial Sequence

<220>

<223> EGFP-Smad4 fusion

<400> 53

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Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50				55					60						
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
65				70					75						80	
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90						95		
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130				135					140						
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145				150					155						160	
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
			165					170						175		
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
		180					185						190			
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
	195					200						205				
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
	210				215					220						
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
225				230					235						240	
Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Asn	Ser	Thr	Met	Asp	
			245					250						255		
Asn	Met	Ser	Ile	Thr	Asn	Thr	Pro	Thr	Ser	Asn	Asp	Ala	Cys	Leu	Ser	
		260						265					270			
Ile	Val	His	Ser	Leu	Met	Cys	His	Arg	Gln	Gly	Gly	Glu	Ser	Glu	Thr	
	275						280					285				
Phe	Ala	Lys	Arg	Ala	Ile	Glu	Ser	Leu	Val	Lys	Lys	Leu	Lys	Glu	Lys	
	290				295						300					
Lys	Asp	Glu	Leu	Asp	Ser	Leu	Ile	Thr	Ala	Ile	Thr	Thr	Asn	Gly	Ala	
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His	Pro	Ser	Lys	Cys	Val	Thr	Ile	Gln	Arg	Thr	Leu	Asp	Gly	Arg	Leu	
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Gln	Val	Ala	Gly	Arg	Lys	Gly	Phe	Pro	His	Val	Ile	Tyr	Ala	Arg	Leu	
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Trp	Arg	Trp	Pro	Asp	Leu	His	Lys	Asn	Glu	Leu	Lys	His	Val	Lys	Tyr	
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Cys	Gln	Tyr	Ala	Phe	Asp	Leu	Lys	Cys	Asp	Ser	Val	Cys	Val	Asn	Pro	
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Tyr	His	Tyr	Glu	Arg	Val	Val	Ser	Pro	Gly	Ile	Asp	Leu	Ser	Gly	Leu	
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Thr	Leu	Gln	Ser	Asn	Ala	Pro	Ser	Ser	Met	Met	Val	Lys	Asp	Glu	Tyr	
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Val	His	Asp	Phe	Glu	Gly	Gln	Pro	Ser	Leu	Ser	Thr	Glu	Gly	His	Ser	

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Ile	Gln	Thr	Ile	Gln	His	Pro	Pro	Ser	Asn	Arg	Ala	Ser	Thr	Glu	Thr		
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Tyr	Ser	Thr	Pro	Ala	Leu	Leu	Ala	Pro	Ser	Glu	Ser	Asn	Ala	Thr	Ser		
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His	Pro	Pro	Met	Pro	Pro	His	Pro	Gly	His	Tyr	Trp	Pro	Val	His	Asn		
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Glu	Leu	Ala	Phe	Gln	Pro	Pro	Ile	Ser	Asn	His	Pro	Ala	Pro	Glu	Tyr		
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Phe	Lys	Val	Pro	Ser	Ser	Cys	Pro	Ile	Val	Thr	Val	Asp	Gly	Tyr	Val		
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Asp	Pro	Ser	Gly	Gly	Asp	Arg	Phe	Cys	Leu	Gly	Gln	Leu	Ser	Asn	Val		
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Val	Gln	Leu	Glu	Cys	Lys	Gly	Glu	Gly	Asp	Val	Trp	Val	Arg	Cys	Leu		
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Ile	Lys	Val	Phe	Asp	Leu	Arg	Gln	Cys	His	Arg	Gln	Met	Gln	Gln	Gln		
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Ala	Ala	Thr	Ala	Gln	Ala	Ala	Ala	Ala	Ala	Gln	Ala	Ala	Ala	Val	Ala		
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Gly	Asn	Ile	Pro	Gly	Pro	Gly	Ser	Val	Gly	Gly	Ile	Ala	Pro	Ala	Ile		
			725						730					735			
Ser	Leu	Ser	Ala	Ala	Ala	Gly	Ile	Gly	Val	Asp	Asp	Leu	Arg	Arg	Leu		
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Cys	Ile	Leu	Arg	Met	Ser	Phe	Val	Lys	Gly	Trp	Gly	Pro	Asp	Tyr	Pro		
	755					760						765					
Arg	Gln	Ser	Ile	Lys	Glu	Thr	Pro	Cys	Trp	Ile	Glu	Ile	His	Leu	His		
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<211> 3120

<212> DNA

<213> Artificial Sequence

<220>

<223> EGFP-Stat5 fusion

<220>

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Glu	Gly	Glu	Gly	Asp	Ala	Thr	Gly	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
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Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
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Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
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cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
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cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
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Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130			135					140					
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Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
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Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
			165					170						175		
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Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
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ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195			200						205				
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
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gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc	720
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
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Gly	Leu	Arg	Ser	Thr	Met	Ala	Gly	Trp	Ile	Gln	Ala	Gln	Gln	Leu	Gln	
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gga	gac	gcg	ctg	cgc	cag	atg	cag	gtg	ctg	tac	ggc	cag	cac	ttc	ccc	816
Gly	Asp	Ala	Leu	Arg	Gln	Met	Gln	Val	Leu	Tyr	Gly	Gln	His	Phe	Pro	
			260				265						270			
atc	gag	gtc	cgg	cac	tac	ttg	gcc	cag	tgg	att	gag	agc	cag	cca	tgg	864

Ile	Glu	Val	Arg	His	Tyr	Leu	Ala	Gln	Trp	Ile	Glu	Ser	Gln	Pro	Trp	
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gat	gcc	att	gac	ttg	gac	aat	ccc	cag	gac	aga	gcc	caa	gcc	acc	cag	912
Asp	Ala	Ile	Asp	Leu	Asp	Asn	Pro	Gln	Asp	Arg	Ala	Gln	Ala	Thr	Gln	
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Leu	Leu	Glu	Gly	Leu	Val	Gln	Glu	Leu	Gln	Lys	Lys	Ala	Glu	His	Gln	
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Val	Gly	Glu	Asp	Gly	Phe	Leu	Leu	Lys	Ile	Lys	Leu	Gly	His	Tyr	Ala	
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acg	cag	ctc	cag	aaa	aca	tat	gac	cgc	tgc	ccc	ctg	gag	ctg	gtc	cgc	1056
Thr	Gln	Leu	Gln	Lys	Thr	Tyr	Asp	Arg	Cys	Pro	Leu	Glu	Leu	Val	Arg	
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Cys	Ile	Arg	His	Ile	Leu	Tyr	Asn	Glu	Gln	Arg	Leu	Val	Arg	Glu	Ala	
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aac	aat	tgc	agc	tct	ccg	gct	ggg	atc	ctg	gtt	gac	gcc	atg	tcc	cag	1152
Asn	Asn	Cys	Ser	Ser	Pro	Ala	Gly	Ile	Leu	Val	Asp	Ala	Met	Ser	Gln	
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Lys	His	Leu	Gln	Ile	Asn	Gln	Thr	Phe	Glu	Glu	Leu	Arg	Leu	Val	Thr	
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Gln	Asp	Thr	Glu	Asn	Glu	Leu	Lys	Lys	Leu	Gln	Gln	Thr	Gln	Glu	Tyr	
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ttc	atc	atc	cag	tac	cag	gag	agc	ctg	agg	atc	caa	gct	cag	ttt	gcc	1296
Phe	Ile	Ile	Gln	Tyr	Gln	Glu	Ser	Leu	Arg	Ile	Gln	Ala	Gln	Phe	Ala	
			420					425					430			
cag	ctg	gcc	cag	ctg	agc	ccc	cag	gag	cgt	ctg	agc	cgg	gag	acg	gcc	1344
Gln	Leu	Ala	Gln	Leu	Ser	Pro	Gln	Glu	Arg	Leu	Ser	Arg	Glu	Thr	Ala	
		435				440						445				
ctc	cag	cag	aag	cag	gtg	tct	ctg	gag	gcc	tgg	ttg	cag	cgt	gag	gca	1392
Leu	Gln	Gln	Lys	Gln	Val	Ser	Leu	Glu	Ala	Trp	Leu	Gln	Arg	Glu	Ala	
		450				455					460					
cag	aca	ctg	cag	cag	tac	cgc	gtg	gag	ctg	gcc	gag	aag	cac	cag	aag	1440
Gln	Thr	Leu	Gln	Gln	Tyr	Arg	Val	Glu	Leu	Ala	Glu	Lys	His	Gln	Lys	
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acc	ctg	cag	ctg	ctg	cgg	aag	cag	cag	acc	atc	ctg	gat	gac	gag		1488
Thr	Leu	Gln	Leu	Leu	Arg	Lys	Gln	Gln	Thr	Ile	Ile	Leu	Asp	Asp	Glu	
				485					490					495		
ctg	atc	cag	tgg	aag	cgg	cgg	cag	cag	ctg	gcc	ggg	aac	ggc	ggg	ccc	1536
Leu	Ile	Gln	Trp	Lys	Arg	Arg	Gln	Gln	Leu	Ala	Gly	Asn	Gly	Gly	Pro	
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ccc	gag	ggc	agc	ctg	gac	gtg	cta	cag	tcc	tgg	tgt	gag	aag	ttg	gcc	1584
Pro	Glu	Gly	Ser	Leu	Asp	Val	Leu	Gln	Ser	Trp	Cys	Glu	Lys	Leu	Ala	
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Cys	Gln	Gln	Leu	Pro	Ile	Pro	Gly	Pro	Val	Glu	Glu	Met	Leu	Ala	Glu	
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Val	Asn	Ala	Thr	Ile	Thr	Asp	Ile	Ile	Ser	Ala	Leu	Val	Thr	Ser	Thr	
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ttc	atc	att	gag	aag	cag	cct	cct	cag	gtc	ctg	aag	acc	cag	acc	aag	1776
Phe	Ile	Ile	Glu	Lys	Gln	Pro	Pro	Gln	Val	Leu	Lys	Thr	Gln	Thr	Lys	
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ttt	gca	gcc	acc	gta	cgc	ctg	ctg	gtg	ggc	ggg	aag	ctg	aac	gtg	cac	1824
Phe	Ala	Ala	Thr	Val	Arg	Leu	Leu	Val	Gly	Gly	Lys	Leu	Asn	Val	His	
		595				600						605				
atg	aat	ccc	ccc	cag	gtg	aag	gcc	acc	atc	atc	agt	gag	cag	cag	gcc	1872

Met	Asn	Pro	Pro	Gln	Val	Lys	Ala	Thr	Ile	Ile	Ser	Glu	Gln	Gln	Ala	
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Leu	Ser	Ala	His	Phe	Arg	Asn	Met	Ser	Leu	Lys	Arg	Ile	Lys	Arg	Ala	
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Ser	Gln	Phe	Asn	Arg	Glu	Asn	Leu	Pro	Gly	Trp	Asn	Tyr	Thr	Phe	Trp	
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cac	gac	ctg	ctc	atc	aac	aag	ccc	gac	ggg	acc	ttc	ttg	ttg	cgc	ttt	2592
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Tyr	Val	Phe	Pro	Asp	Arg	Pro	Lys	Asp	Glu	Val	Phe	Ser	Lys	Tyr	Tyr	
				915										925		
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Thr	Pro	Val	Leu	Ala	Lys	Ala	Val	Asp	Gly	Tyr	Val	Lys	Pro	Gln	Ile	
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Ser	Ser	Ala	Thr	Tyr	Met	Asp	Gln	Ala	Pro	Ser	Pro	Ala	Val	Cys	Pro		
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cag	gct	ccc	tat	aac	atg	tac	cca	cag	aac	cct	gac	cat	gta	ctc	gat	2976	
Gln	Ala	Pro	Tyr	Asn	Met	Tyr	Pro	Gln	Asn	Pro	Asp	His	Val	Leu	Asp		
			980					985					990				
cag	gat	gga	gaa	ttc	gac	ctg	gat	gag	acc	atg	gat	gtg	gcc	agg	cac	3024	
Gln	Asp	Gly	Glu	Phe	Asp	Leu	Asp	Glu	Thr	Met	Asp	Val	Ala	Arg	His		
		995					1000					1005					
gtg	gag	gaa	ctc	tta	cgc	cga	cca	atg	gac	agt	ctt	gac	tcc	cgc		3069	
Val	Glu	Glu	Leu	Leu	Arg	Arg	Pro	Met	Asp	Ser	Leu	Asp	Ser	Arg			
	1010					1015					1020						
ctc	tcg	ccc	cct	gcc	ggt	ctt	ttc	acc	tct	gcc	aga	ggc	tcc	ctc		3114	
Leu	Ser	Pro	Pro	Ala	Gly	Leu	Phe	Thr	Ser	Ala	Arg	Gly	Ser	Leu			
	1025					1030					1035						
tca	tga															3120	
Ser																	

<210> 55

<211> 1039

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-Stat5 fusion

<400> 55

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1			5						10					15			
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
		20					25						30				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
	35					40						45					
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
	50				55						60						
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys		
65				70					75					80			
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
		85						90					95				
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
		100					105						110				
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
	115					120						125					
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130				135					140							
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145				150					155					160			
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
		165					170						175				
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly		
	180						185					190					
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu		
	195					200						205					

Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe
210						215					220				
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser
225					230					235					240
Gly	Leu	Arg	Ser	Thr	Met	Ala	Gly	Trp	Ile	Gln	Ala	Gln	Gln	Leu	Gln
				245					250					255	
Gly	Asp	Ala	Leu	Arg	Gln	Met	Gln	Val	Leu	Tyr	Gly	Gln	His	Phe	Pro
			260					265					270		
Ile	Glu	Val	Arg	His	Tyr	Leu	Ala	Gln	Trp	Ile	Glu	Ser	Gln	Pro	Trp
		275					280					285			
Asp	Ala	Ile	Asp	Leu	Asp	Asn	Pro	Gln	Asp	Arg	Ala	Gln	Ala	Thr	Gln
290						295					300				
Leu	Leu	Glu	Gly	Leu	Val	Gln	Glu	Leu	Gln	Lys	Lys	Ala	Glu	His	Gln
305					310					315					320
Val	Gly	Glu	Asp	Gly	Phe	Leu	Leu	Lys	Ile	Lys	Leu	Gly	His	Tyr	Ala
				325					330					335	
Thr	Gln	Leu	Gln	Lys	Thr	Tyr	Asp	Arg	Cys	Pro	Leu	Glu	Leu	Val	Arg
			340				345						350		
Cys	Ile	Arg	His	Ile	Leu	Tyr	Asn	Glu	Gln	Arg	Leu	Val	Arg	Glu	Ala
		355					360					365			
Asn	Asn	Cys	Ser	Ser	Pro	Ala	Gly	Ile	Leu	Val	Asp	Ala	Met	Ser	Gln
		370				375					380				
Lys	His	Leu	Gln	Ile	Asn	Gln	Thr	Phe	Glu	Glu	Leu	Arg	Leu	Val	Thr
385					390					395					400
Gln	Asp	Thr	Glu	Asn	Glu	Leu	Lys	Lys	Leu	Gln	Gln	Thr	Gln	Glu	Tyr
				405					410					415	
Phe	Ile	Ile	Gln	Tyr	Gln	Glu	Ser	Leu	Arg	Ile	Gln	Ala	Gln	Phe	Ala
			420					425					430		
Gln	Leu	Ala	Gln	Leu	Ser	Pro	Gln	Glu	Arg	Leu	Ser	Arg	Glu	Thr	Ala
		435					440					445			
Leu	Gln	Gln	Lys	Gln	Val	Ser	Leu	Glu	Ala	Trp	Leu	Gln	Arg	Glu	Ala
		450				455					460				
Gln	Thr	Leu	Gln	Gln	Tyr	Arg	Val	Glu	Leu	Ala	Glu	Lys	His	Gln	Lys
465					470				475						480
Thr	Leu	Gln	Leu	Leu	Arg	Lys	Gln	Gln	Thr	Ile	Ile	Leu	Asp	Asp	Glu
				485					490					495	
Leu	Ile	Gln	Trp	Lys	Arg	Arg	Gln	Gln	Leu	Ala	Gly	Asn	Gly	Gly	Pro
			500					505					510		
Pro	Glu	Gly	Ser	Leu	Asp	Val	Leu	Gln	Ser	Trp	Cys	Glu	Lys	Leu	Ala
		515				520						525			
Glu	Ile	Ile	Trp	Gln	Asn	Arg	Gln	Gln	Ile	Arg	Arg	Ala	Glu	His	Leu
		530				535					540				
Cys	Gln	Gln	Leu	Pro	Ile	Pro	Gly	Pro	Val	Glu	Glu	Met	Leu	Ala	Glu
545					550					555					560
Val	Asn	Ala	Thr	Ile	Thr	Asp	Ile	Ile	Ser	Ala	Leu	Val	Thr	Ser	Thr
				565					570					575	
Phe	Ile	Ile	Glu	Lys	Gln	Pro	Pro	Gln	Val	Leu	Lys	Thr	Gln	Thr	Lys
			580					585					590		
Phe	Ala	Ala	Thr	Val	Arg	Leu	Leu	Val	Gly	Gly	Lys	Leu	Asn	Val	His
		595					600					605			
Met	Asn	Pro	Pro	Gln	Val	Lys	Ala	Thr	Ile	Ile	Ser	Glu	Gln	Gln	Ala
		610				615					620				
Lys	Ser	Leu	Leu	Lys	Asn	Glu	Asn	Thr	Arg	Asn	Glu	Cys	Ser	Gly	Glu
625					630					635					640
Ile	Leu	Asn	Asn	Cys	Cys	Val	Met	Glu	Tyr	His	Gln	Ala	Thr	Gly	Thr
				645					650					655	
Leu	Ser	Ala	His	Phe	Arg	Asn	Met	Ser	Leu	Lys	Arg	Ile	Lys	Arg	Ala
			660					665					670		
Asp	Arg	Arg	Gly	Ala	Glu	Ser	Val	Thr	Glu	Glu	Lys	Phe	Thr	Val	Leu
		675					680					685			
Phe	Glu	Ser	Gln	Phe	Ser	Val	Gly	Ser	Asn	Glu	Leu	Val	Phe	Gln	Val
		690				695					700				
Lys	Thr	Leu	Ser	Leu	Pro	Val	Val	Val	Ile	Val	His	Gly	Ser	Gln	Asp

705					710					715				720
His	Asn	Ala	Thr	Ala	Thr	Val	Leu	Trp	Asp	Asn	Ala	Phe	Ala	Glu
				725					730					735
Gly	Arg	Val	Pro	Phe	Ala	Val	Pro	Asp	Lys	Val	Leu	Trp	Pro	Gln
			740					745					750	
Cys	Glu	Ala	Leu	Asn	Met	Lys	Phe	Lys	Ala	Glu	Val	Gln	Ser	Asn
		755				760						765		
Gly	Leu	Thr	Lys	Glu	Asn	Leu	Val	Phe	Leu	Ala	Gln	Lys	Leu	Phe
	770					775					780			
Asn	Ser	Ser	Ser	His	Leu	Glu	Asp	Tyr	Ser	Gly	Leu	Ser	Val	Ser
785					790				795					800
Ser	Gln	Phe	Asn	Arg	Glu	Asn	Leu	Pro	Gly	Trp	Asn	Tyr	Thr	Phe
			805					810						815
Gln	Trp	Phe	Asp	Gly	Val	Met	Glu	Val	Leu	Lys	Lys	His	His	Lys
			820					825					830	
His	Trp	Asn	Asp	Gly	Ala	Ile	Leu	Gly	Phe	Val	Asn	Lys	Gln	Gln
		835					840					845		
His	Asp	Leu	Leu	Ile	Asn	Lys	Pro	Asp	Gly	Thr	Phe	Leu	Leu	Arg
	850					855					860			
Ser	Asp	Ser	Glu	Ile	Gly	Gly	Ile	Thr	Ile	Ala	Trp	Lys	Phe	Asp
865					870					875				880
Pro	Glu	Arg	Asn	Leu	Trp	Asn	Leu	Lys	Pro	Phe	Thr	Thr	Arg	Asp
			885					890						895
Ser	Ile	Arg	Ser	Leu	Ala	Asp	Arg	Leu	Gly	Asp	Leu	Ser	Tyr	Leu
			900					905					910	
Tyr	Val	Phe	Pro	Asp	Arg	Pro	Lys	Asp	Glu	Val	Phe	Ser	Lys	Tyr
		915					920					925		
Thr	Pro	Val	Leu	Ala	Lys	Ala	Val	Asp	Gly	Tyr	Val	Lys	Pro	Gln
	930					935					940			
Lys	Gln	Val	Val	Pro	Glu	Phe	Val	Asn	Ala	Ser	Ala	Asp	Ala	Gly
945					950					955				960
Ser	Ser	Ala	Thr	Tyr	Met	Asp	Gln	Ala	Pro	Ser	Pro	Ala	Val	Cys
			965					970						975
Gln	Ala	Pro	Tyr	Asn	Met	Tyr	Pro	Gln	Asn	Pro	Asp	His	Val	Leu
		980						985					990	
Gln	Asp	Gly	Glu	Phe	Asp	Leu	Asp	Glu	Thr	Met	Asp	Val	Ala	Arg
		995					1000					1005		
Val	Glu	Glu	Leu	Leu	Arg	Arg	Pro	Met	Asp	Ser	Leu	Asp	Ser	Arg
	1010					1015					1020			
Leu	Ser	Pro	Pro	Ala	Gly	Leu	Phe	Thr	Ser	Ala	Arg	Gly	Ser	Leu
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Ser														

<210> 56

<211> 1875

<212> DNA

<213> Artificial Sequence

<220>

<223> mERK1-F64L-S65T-GFP fusion

<220>

<221> CDS



<222> (1)..(1872)

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1                               5                               10          15
gga act gct ggg gtc gtc ccg gtg gtc ccc ggg gag gtg gag gtg gtg      96
Gly Thr Ala Gly Val Val Pro Val Val Pro Gly Glu Val Glu Val Val
                               20                               25          30
aag ggg cag cca ttc gat gtg ggc cca cgc tac acg cag ctg cag tac      144
Lys Gly Gln Pro Phe Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr
                               35                               40          45
atc ggc gag ggc gcg tac ggc atg gtc agc tca gct tat gac cac gtg      192
Ile Gly Glu Gly Ala Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val
                               50                               55          60
cgc aag acc aga gtg gcc atc aag aag atc agc ccc ttt gag cat caa      240
Arg Lys Thr Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln
65                               70                               75          80
acc tac tgt cag cgc acg ctg agg gag atc cag atc ttg ctg cga ttc      288
Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe
                               85                               90          95
cgc cat gag aat gtt ata ggc atc cga gac atc ctc aga gcg ccc acc      336
Arg His Glu Asn Val Ile Gly Ile Arg Asp Ile Leu Arg Ala Pro Thr
                               100                              105          110
ctg gaa gcc atg aga gat gtt tac att gtt cag gac ctc atg gag aca      384
Leu Glu Ala Met Arg Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr
                               115                              120          125
gac ctg tac aag ctg ctt aaa agc cag cag ctg agc aat gac cac atc      432
Asp Leu Tyr Lys Leu Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile
130                              135                              140
tgc tac ttc ctc tac cag atc ctc cgg ggc ctc aag tat ata cac tca      480
Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser
145                              150                              155          160
gcc aat gtg ctg cac cgg gac ctg aag cct tcc aat ctg ctt atc aac      528
Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Ile Asn
                               165                              170          175
acc acc tgc gac ctt aag atc tgt gat ttt ggc ctg gcc cgg att gct      576
Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala
                               180                              185          190
gac cct gag cac gac cac act ggc ttt ctg acg gag tat gtg gcc aca      624
Asp Pro Glu His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr
                               195                              200          205
cgc tgg tac cga gcc cca gag atc atg ctt aat tcc aag ggc tac acc      672
Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr
210                              215                              220
aaa tcc atc gac atc tgg tct gtg ggc tgc att ctg gct gag atg ctc      720
Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu
225                              230                              235          240
tcc aac cgg ccc atc ttc ccc ggc aag cac tac ctg gac cag ctc aac      768
Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn
                               245                              250          255
cac att cta ggt atc ttg ggt tcc cca tcc cag gag gac ctt aat tgc      816
His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys
                               260                              265          270
atc att aac atg aag gcc cga aac tac ctg cag tct ctg ccc tcg aaa      864
Ile Ile Asn Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys
275                              280                              285
acc aag gtg gct tgg gcc aag ctc ttt cct aaa tct gac tcc aaa gct      912
Thr Lys Val Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala
290                              295                              300
ctt gac ctg ctg gac cgg atg tta acc ttc aac cca aac aag cgc atc      960

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Leu	Asp	Leu	Leu	Asp	Arg	Met	Leu	Thr	Phe	Asn	Pro	Asn	Lys	Arg	Ile	
305					310					315					320	
aca	gta	gag	gaa	gcg	ctg	gct	cac	cct	tac	ctg	gaa	cag	tac	tac	gat	1008
Thr	Val	Glu	Glu	Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp	
				325					330						335	
ccg	aca	gat	gag	cca	gtg	gcc	gag	gag	cca	ttc	acc	ttc	gac	atg	gag	1056
Pro	Thr	Asp		Pro	Val	Ala	Glu	Glu	Pro	Phe	Thr	Phe	Asp	Met	Glu	
				340					345						350	
ctg	gat	gac	ctc	ccc	aag	gag	cgg	ctg	aag	gag	ttg	atc	ttc	cag	gag	1104
Leu	Asp	Asp	Leu	Pro	Lys	Glu	Arg	Leu	Lys	Glu	Leu	Ile	Phe	Gln	Glu	
				355					360						365	
aca	gcc	cgc	ttc	cag	cca	ggg	gcg	cca	gag	ggc	ccc	ggg	cgc	gcc	atg	1152
Thr	Ala	Arg	Phe	Gln	Pro	Gly	Ala	Pro	Glu	Gly	Pro	Gly	Arg	Ala	Met	
				370											380	
agt	aaa	gga	gaa	gaa	ctt	ttc	act	gga	gtt	gtc	cca	att	ctt	gtt	gaa	1200
Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	
385					390										400	
tta	gat	ggc	gat	gtt	aat	ggg	caa	aaa	ttc	tct	gtt	agt	gga	gag	ggt	1248
Leu	Asp	Gly	Asp	Val	Asn	Gly	Gln	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	
				405					410						415	
gaa	ggt	gat	gca	aca	tac	gga	aaa	ctt	acc	ctt	aaa	ttt	att	tgc	act	1296
Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	
				420					425						430	
act	ggg	aag	cta	cct	gtt	cca	tgg	cca	acg	ctt	gtc	act	act	ctc	act	1344
Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	
				435											445	
tat	ggt	gtt	caa	tgc	ttt	tct	aga	tac	cca	gat	cat	atg	aaa	cag	cat	1392
Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	
				450											460	
gac	ttt	ttc	aag	agt	gcc	atg	ccc	gaa	ggt	tat	gta	cag	gaa	aga	act	1440
Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	
465					470										480	
ata	ttt	tac	aaa	gat	gac	ggg	aac	tac	aag	aca	cgt	gct	gaa	gtc	aag	1488
Ile	Phe	Tyr	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	
				485					490						495	
ttt	gaa	ggt	gat	acc	ctt	gtt	aat	aga	atc	gag	tta	aaa	ggt	att	gat	1536
Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	
				500					505						510	
ttt	aaa	gaa	gat	gga	aac	att	ctt	gga	cac	aaa	atg	gaa	tac	aat	tat	1584
Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Met	Glu	Tyr	Asn	Tyr	
				515					520						525	
aac	tca	cat	aat	gta	tac	atc	atg	gca	gac	aaa	cca	aag	aat	ggc	atc	1632
Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Pro	Lys	Asn	Gly	Ile	
				530											540	
aaa	gtt	aac	ttc	aaa	att	aga	cac	aac	att	aaa	gat	gga	agc	gtt	caa	1680
Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Lys	Asp	Gly	Ser	Val	Gln	
545					550										560	
tta	gca	gac	cat	tat	caa	caa	aat	act	cca	att	ggc	gat	ggc	cct	gtc	1728
Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	
				565					570						575	
ctt	tta	cca	gac	aac	cat	tac	ctg	tcc	acg	caa	tct	gcc	ctt	tcc	aaa	1776
Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	
				580					585						590	
gat	ccc	aac	gaa	aag	aga	gat	cac	atg	atc	ctt	ctt	gag	ttt	gta	aca	1824
Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Leu	Leu	Glu	Phe	Val	Thr	
				595											605	
gct	gct	ggg	att	aca	cat	ggc	atg	gat	gaa	cta	tac	aaa	cct	cag	gag	1872
Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Pro	Gln	Glu	
				610											620	
taa																1875

<210> 57

<211> 624

<212> PRT

<213> Artificial Sequence

<220>

<223> mERK1-F64L-S65T-GFP fusion

<400> 57

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20      25      30
Lys Gly Gln Pro Phe Asp Val Gly Pro Arg Tyr Thr Gln Leu Gln Tyr
35      40      45
Ile Gly Glu Gly Ala Tyr Gly Met Val Ser Ser Ala Tyr Asp His Val
50      55      60
Arg Lys Thr Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln
65      70      75      80
Thr Tyr Cys Gln Arg Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe
85      90      95
Arg His Glu Asn Val Ile Gly Ile Arg Asp Ile Leu Arg Ala Pro Thr
100     105     110
Leu Glu Ala Met Arg Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr
115     120     125
Asp Leu Tyr Lys Leu Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile
130     135     140
Cys Tyr Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser
145     150     155     160
Ala Asn Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Ile Asn
165     170     175
Thr Thr Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala
180     185     190
Asp Pro Glu His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr
195     200     205
Arg Trp Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr
210     215     220
Lys Ser Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu
225     230     235     240
Ser Asn Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn
245     250     255
His Ile Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys
260     265     270
Ile Ile Asn Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys
275     280     285
Thr Lys Val Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala
290     295     300
Leu Asp Leu Leu Asp Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile
305     310     315     320
Thr Val Glu Glu Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp
325     330     335
Pro Thr Asp Glu Pro Val Ala Glu Glu Pro Phe Thr Phe Asp Met Glu
340     345     350
Leu Asp Asp Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu
355     360     365

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Thr	Ala	Arg	Phe	Gln	Pro	Gly	Ala	Pro	Glu	Gly	Pro	Gly	Arg	Ala	Met
370						375					380				
Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu
385					390					395					400
Leu	Asp	Gly	Asp	Val	Asn	Gly	Gln	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly
				405					410					415	
Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr
			420					425					430		
Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr
			435				440					445			
Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His
						455					460				
Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr
465					470					475					480
Ile	Phe	Tyr	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys
				485					490					495	
Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp
			500					505					510		
Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Met	Glu	Tyr	Asn	Tyr
		515					520					525			
Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Pro	Lys	Asn	Gly	Ile
		530				535					540				
Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Lys	Asp	Gly	Ser	Val	Gln
545					550					555					560
Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val
				565					570					575	
Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys
			580					585					590		
Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Leu	Leu	Glu	Phe	Val	Thr
		595					600					605			
Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Pro	Gln	Glu
610						615					620				

<210> 58

<211> 1815

<212> DNA

<213> Artificial Sequence

<220>

<223> Erk2-EGFP fusion

<220>

<221> CDS

<222> (1)..(1812)

<400> 58

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Met	Ala	Ala	Ala	Ala	Ala	Ala	Gly	Pro	Glu	Met	Val	Arg	Gly	Gln	Val	
1			5					10					15			
ttc	gac	gtg	ggg	ccg	cgc	tac	act	aat	ctc	tcg	tac	atc	gga	gaa	ggc	96
Phe	Asp	Val	Gly	Pro	Arg	Tyr	Thr	Asn	Leu	Ser	Tyr	Ile	Gly	Glu	Gly	
			20					25					30			

gcc	tac	ggc	atg	gtt	tgt	tct	gct	tat	gat	aat	ctc	aac	aaa	gtt	cga	144
Ala	Tyr	Gly	Met	Val	Cys	Ser	Ala	Tyr	Asp	Asn	Leu	Asn	Lys	Val	Arg	
		35					40					45				
gtt	gct	atc	aag	aaa	atc	agt	cct	ttt	gag	cac	cag	acc	tac	tgt	cag	192
Val	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe	Glu	His	Gln	Thr	Tyr	Cys	Gln	
		50					55				60					
aga	acc	ctg	aga	gag	ata	aaa	atc	cta	ctg	cgc	ttc	aga	cat	gag	aac	240
Arg	Thr	Leu	Arg	Glu	Ile	Lys	Ile	Leu	Leu	Arg	Phe	Arg	His	Glu	Asn	
		65				70				75					80	
atc	atc	ggc	atc	aat	gac	atc	atc	cgg	gca	cca	acc	att	gag	cag	atg	288
Ile	Ile	Gly	Ile	Asn	Asp	Ile	Ile	Arg	Ala	Pro	Thr	Ile	Glu	Gln	Met	
				85				90						95		
aaa	gat	gta	tat	ata	gta	cag	gac	ctc	atg	gag	aca	gat	ctt	tac	aag	336
Lys	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	Met	Glu	Thr	Asp	Leu	Tyr	Lys	
			100					105					110			
ctc	ttg	aag	aca	cag	cac	ctc	agc	aat	gat	cat	atc	tgc	tat	ttt	ctt	384
Leu	Leu	Lys	Thr	Gln	His	Leu	Ser	Asn	Asp	His	Ile	Cys	Tyr	Phe	Leu	
		115					120					125				
tat	cag	atc	ctg	aga	gga	tta	aag	tat	ata	cat	tca	gct	aat	gtt	ctg	432
Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asn	Val	Leu	
		130				135					140					
cac	cgt	gac	ctc	aag	cct	tcc	aac	ctc	ctg	ctg	aac	acc	act	tgt	gat	480
His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Leu	Leu	Asn	Thr	Thr	Cys	Asp	
				150				155						160		
ctc	aag	atc	tgt	gac	ttt	ggc	ctt	gcc	cgt	gtt	gca	gat	cca	gac	cat	528
Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Val	Ala	Asp	Pro	Asp	His	
			165					170						175		
gat	cat	aca	ggg	ttc	ttg	aca	gag	tat	gta	gcc	acg	cgt	tgg	tac	aga	576
Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	
			180					185					190			
gct	cca	gaa	att	atg	ttg	aat	tcc	aag	ggt	tat	acc	aag	tcc	att	gat	624
Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr	Lys	Ser	Ile	Asp	
		195					200					205				
att	tgg	tct	gtg	ggc	tgc	atc	ctg	gca	gag	atg	cta	tcc	aac	agg	cct	672
Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu	Ser	Asn	Arg	Pro	
		210			215						220					
atc	ttc	cca	gga	aag	cat	tac	ctt	gac	cag	ctg	aat	cac	atc	ctg	ggt	720
Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn	His	Ile	Leu	Gly	
				230					235					240		
att	ctt	gga	tct	cca	tca	cag	gaa	gat	ctg	aat	tgt	ata	ata	aat	tta	768
Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys	Ile	Ile	Asn	Leu	
			245					250						255		
aaa	gct	aga	aac	tat	ttg	ctt	tct	ctc	ccg	cac	aaa	aat	aag	gtg	ccg	816
Lys	Ala	Arg	Asn	Tyr	Leu	Leu	Ser	Leu	Pro	His	Lys	Asn	Lys	Val	Pro	
			260					265					270			
tgg	aac	agg	ttg	ttc	cca	aac	gct	gac	tcc	aaa	gct	ctg	gat	tta	ctg	864
Trp	Asn	Arg	Leu	Phe	Pro	Asn	Ala	Asp	Ser	Lys	Ala	Leu	Asp	Leu	Leu	
		275					280					285				
gat	aaa	atg	ttg	aca	ttt	aac	cct	cac	aag	agg	att	gaa	gtt	gaa	cag	912
Asp	Lys	Met	Leu	Thr	Phe	Asn	Pro	His	Lys	Arg	Ile	Glu	Val	Glu	Gln	
		290				295					300					
gct	ctg	gcc	cac	ccg	tac	ctg	gag	cag	tat	tat	gac	cca	agt	gat	gag	960
Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp	Pro	Ser	Asp	Glu	
		305			310				315						320	
ccc	att	gct	gaa	gca	cca	ttc	aag	ttt	gac	atg	gag	ctg	gac	gac	tta	1008
Pro	Ile	Ala	Glu	Ala	Pro	Phe	Lys	Phe	Asp	Met	Glu	Leu	Asp	Asp	Leu	
			325					330						335		
cct	aag	gag	aag	ctc	aaa	gaa	ctc	att	ttt	gaa	gag	act	gct	cga	ttc	1056
Pro	Lys	Glu	Lys	Leu	Lys	Glu	Leu	Ile	Phe	Glu	Glu	Thr	Ala	Arg	Phe	
			340					345					350			
cag	cca	gga	tac	aga	tct	atg	gat	cca	ccg	gtc	gcc	acc	atg	gtg	agc	1104
Gln	Pro	Gly	Tyr	Arg	Ser	Met	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	
		355					360					365				

aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg	1152
Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu	
370 375 380	
gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag	1200
Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu	
385 390 395 400	
ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc	1248
Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr	
405 410 415	
ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tac	1296
Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr	
420 425 430	
ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag cac gac	1344
Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp	
435 440 445	
ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc	1392
Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile	
450 455 460	
ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc	1440
Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe	
465 470 475 480	
gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc	1488
Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe	
485 490 495	
aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac aac	1536
Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn	
500 505 510	
agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag	1584
Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys	
515 520 525	
gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc	1632
Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu	
530 535 540	
gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg	1680
Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu	
545 550 555 560	
ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac	1728
Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp	
565 570 575	
ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc	1776
Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala	
580 585 590	
gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa	1815
Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
595 600	

<210> 59

<211> 604

<212> PRT

<213> Artificial Sequence

<220>

<223> Erk2-EGFP fusion

<400> 59

Met Ala Ala Ala Ala Ala Ala Gly Pro Glu Met Val Arg Gly Gln Val

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Phe	Asp	Val	Gly	Pro	Arg	Tyr	Thr	Asn	Leu	Ser	Tyr	Ile	Gly
			20					25					30
Ala	Tyr	Gly	Met	Val	Cys	Ser	Ala	Tyr	Asp	Asn	Leu	Asn	Lys
		35					40					45	
Val	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe	Glu	His	Gln	Thr	Tyr
		50				55					60		
Arg	Thr	Leu	Arg	Glu	Ile	Lys	Ile	Leu	Leu	Arg	Phe	Arg	His
65					70					75			80
Ile	Ile	Gly	Ile	Asn	Asp	Ile	Ile	Arg	Ala	Pro	Thr	Ile	Glu
				85					90				95
Lys	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	Met	Glu	Thr	Asp	Leu
		100						105				110	
Leu	Leu	Lys	Thr	Gln	His	Leu	Ser	Asn	Asp	His	Ile	Cys	Tyr
		115					120					125	
Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asn
		130				135					140		
His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Leu	Leu	Asn	Thr	Thr
145					150					155			160
Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Val	Ala	Asp	Pro
			165						170				175
Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr	Arg	Trp
		180						185				190	
Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr	Lys	Ser
		195					200					205	
Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu	Ser	Asn
	210					215						220	
Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn	His	Ile
225					230					235			240
Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys	Ile	Ile
			245						250				255
Lys	Ala	Arg	Asn	Tyr	Leu	Leu	Ser	Leu	Pro	His	Lys	Asn	Lys
			260					265				270	
Trp	Asn	Arg	Leu	Phe	Pro	Asn	Ala	Asp	Ser	Lys	Ala	Leu	Asp
	275						280					285	
Asp	Lys	Met	Leu	Thr	Phe	Asn	Pro	His	Lys	Arg	Ile	Glu	Val
	290					295					300		
Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp	Pro	Ser
305					310					315			320
Pro	Ile	Ala	Glu	Ala	Pro	Phe	Lys	Phe	Asp	Met	Glu	Leu	Asp
			325						330				335
Pro	Lys	Glu	Lys	Leu	Lys	Glu	Leu	Ile	Phe	Glu	Glu	Thr	Ala
			340					345					350
Gln	Pro	Gly	Tyr	Arg	Ser	Met	Asp	Pro	Pro	Val	Ala	Thr	Met
	355						360					365	
Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
	370					375					380		
Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
385					390					395			400
Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
			405						410				415
Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu
		420						425				430	
Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln
	435						440					445	
Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
	450					455					460		
Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
465				470						475			480
Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
			485						490				495
Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
			500					505					510

Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys
		515					520					525			
Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu
	530					535					540				
Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu
545					550					555					560
Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp
			565						570					575	
Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala
		580					585						590		
Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys				
	595						600								

<210> 60

<211> 2511

<212> DNA

<213> Artificial Sequence

<220>

<223> Grk5-EGFP fusion

<220>

<221> CDS

<222> (1)..(2508)

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Met	Glu	Leu	Glu	Asn	Ile	Val	Ala	Asn	Thr	Val	Leu	Leu	Lys	Ala	Arg				
1			5						10				15						
gaa	ggg	ggc	gga	gga	aag	cgc	aaa	ggg	aaa	agc	aag	aag	tgg	aaa	gaa				96
Glu	Gly	Gly	Gly	Gly	Lys	Arg	Lys	Gly	Lys	Ser	Lys	Lys	Trp	Lys	Glu				
		20						25					30						
atc	ctg	aag	ttc	cct	cac	att	agc	cag	tgt	gaa	gac	ctc	cga	agg	acc				144
Ile	Leu	Lys	Phe	Pro	His	Ile	Ser	Gln	Cys	Glu	Asp	Leu	Arg	Arg	Thr				
		35					40					45							
ata	gac	aga	gat	tac	tgc	agt	tta	tgt	gac	aag	cag	cca	atc	ggg	agg				192
Ile	Asp	Arg	Asp	Tyr	Cys	Ser	Leu	Cys	Asp	Lys	Gln	Pro	Ile	Gly	Arg				
	50					55					60								
ctg	ctt	ttc	cgg	cag	ttt	tgt	gaa	acc	agg	cct	ggg	ctg	gag	tgt	tac				240
Leu	Leu	Phe	Arg	Gln	Phe	Cys	Glu	Thr	Arg	Pro	Gly	Leu	Glu	Cys	Tyr				
65				70					75					80					
att	cag	ttc	ctg	gac	tcc	gtg	gca	gaa	tat	gaa	gtt	act	cca	gat	gaa				288
Ile	Gln	Phe	Leu	Asp	Ser	Val	Ala	Glu	Tyr	Glu	Val	Thr	Pro	Asp	Glu				
			85						90					95					
aaa	ctg	gga	gag	aaa	ggg	aag	gaa	att	atg	acc	aag	tac	ctc	acc	cca				336
Lys	Leu	Gly	Glu	Lys	Gly	Lys	Glu	Ile	Met	Thr	Lys	Tyr	Leu	Thr	Pro				
		100						105					110						
aag	tcc	cct	gtt	ttc	ata	gcc	caa	gtt	ggc	caa	gac	ctg	gtc	tcc	cag				384
Lys	Ser	Pro	Val	Phe	Ile	Ala	Gln	Val	Gly	Gln	Asp	Leu	Val	Ser	Gln				
		115					120					125							
acg	gag	gag	aag	ctc	cta	cag	aag	ccg	tgc	aaa	gaa	ctc	ttt	tct	gcc				432
Thr	Glu	Glu	Lys	Leu	Leu	Gln	Lys	Pro	Cys	Lys	Glu	Leu	Phe	Ser	Ala				



130	135	140	
tgt gca cag tct gtc cac gag tac ctg agg gga gaa cca ttc cac gaa			480
Cys Ala Gln Ser Val His Glu Tyr Leu Arg Gly Glu Pro Phe His Glu			
145	150	155	160
tat ctg gac agc atg ttt ttt gac cgc ttt ctc cag tgg aag tgg ttg			528
Tyr Leu Asp Ser Met Phe Phe Asp Arg Phe Leu Gln Trp Lys Trp Leu			
165	170		175
gaa agg caa ccg gtg acc aaa aac act ttc agg cag tat cga gtg cta			576
Glu Arg Gln Pro Val Thr Lys Asn Thr Phe Arg Gln Tyr Arg Val Leu			
180	185		190
gga aaa ggg ggc ttc ggg gag gtc tgt gcc tgc cag gtt cgg gcc acg			624
Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Cys Gln Val Arg Ala Thr			
195	200		205
ggt aaa atg tat gcc tgc aag cgc ttg gag aag aag agg atc aaa aag			672
Gly Lys Met Tyr Ala Cys Lys Arg Leu Glu Lys Lys Arg Ile Lys Lys			
210	215		220
agg aaa ggg gag tcc atg gcc ctc aat gag aag cag atc ctc gag aag			720
Arg Lys Gly Glu Ser Met Ala Leu Asn Glu Lys Gln Ile Leu Glu Lys			
225	230		235
gtc aac agt cag ttt gtg gtc aac ctg gcc tat gcc tac gag acc aag			768
Val Asn Ser Gln Phe Val Val Asn Leu Ala Tyr Ala Tyr Glu Thr Lys			
245	250		255
gat gca ctg tgc ttg gtc ctg acc atc atg aat ggg ggt gac ctg aag			816
Asp Ala Leu Cys Leu Val Leu Thr Ile Met Asn Gly Gly Asp Leu Lys			
260	265		270
ttc cac atc tac aac atg ggc aac cct ggc ttc gag gag cgg gcc			864
Phe His Ile Tyr Asn Met Gly Asn Pro Gly Phe Glu Glu Glu Arg Ala			
275	280		285
ttg ttt tat gcg gca gag atc ctc tgc ggc tta gaa gac ctc cac cgt			912
Leu Phe Tyr Ala Ala Glu Ile Leu Cys Gly Leu Glu Asp Leu His Arg			
290	295		300
gag aac acc gtc tac cga gat ctg aaa cct gaa aac atc ctg tta gat			960
Glu Asn Thr Val Tyr Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp			
305	310		315
gat tat ggc cac att agg atc tca gac ctg ggc ttg gct gtg aag atc			1008
Asp Tyr Gly His Ile Arg Ile Ser Asp Leu Gly Leu Ala Val Lys Ile			
325	330		335
ccc gag gga gac ctg atc cgc ggc cgg gtg ggc act gtt ggc tac atg			1056
Pro Glu Gly Asp Leu Ile Arg Gly Arg Val Gly Thr Val Gly Tyr Met			
340	345		350
gcc ccc gaa gtc ctg aac aac cag agg tac ggc ctg agc ccc gac tac			1104
Ala Pro Glu Val Leu Asn Asn Gln Arg Tyr Gly Leu Ser Pro Asp Tyr			
355	360		365
tggt ggc ctt ggc tgc ctc atc tat gag atg atc gag ggc cag tcg ccg			1152
Trp Gly Leu Gly Cys Leu Ile Tyr Glu Met Ile Glu Gly Gln Ser Pro			
370	375		380
ttc cgc ggc cgt aag gag aag gtg aag cgg gag gag gtg gac cgc cgg			1200
Phe Arg Gly Arg Lys Glu Lys Val Lys Arg Glu Glu Val Asp Arg Arg			
385	390		395
gtc ctg gag acg gag gag gtg tac tcc cac aag ttc tcc gag gag gcc			1248
Val Leu Glu Thr Glu Glu Val Tyr Ser His Lys Phe Ser Glu Glu Ala			
405	410		415
aag tcc atc tgc aag atg ctg ctc acg aaa gat gcg aag cag agg ctg			1296
Lys Ser Ile Cys Lys Met Leu Leu Thr Lys Asp Ala Lys Gln Arg Leu			
420	425		430
ggc tgc cag gag gag ggg gct gca gag gtc aag aga cac ccc ttc ttc			1344
Gly Cys Gln Glu Glu Gly Ala Ala Glu Val Lys Arg His Pro Phe Phe			
435	440		445
agg aac atg aac ttc aag cgc tta gaa gcc ggg atg ttg gac cct ccc			1392
Arg Asn Met Asn Phe Lys Arg Leu Glu Ala Gly Met Leu Asp Pro Pro			
450	455		460
ttc gtt cca gac ccc cgc gct gtg tac tgt aag gac gtg ctg gac atc			1440
Phe Val Pro Asp Pro Arg Ala Val Tyr Cys Lys Asp Val Leu Asp Ile			

465					470					475				480		
gag	cag	ttc	tcc	act	gtg	aag	ggc	gtc	aat	ctg	gac	cac	aca	gac	gac	1488
Glu	Gln	Phe	Ser	Thr	Val	Lys	Gly	Val	Asn	Leu	Asp	His	Thr	Asp	Asp	
				485					490					495		
gac	ttc	tac	tcc	aag	ttc	tcc	acg	ggc	tct	gtg	tcc	atc	cca	tgg	caa	1536
Asp	Phe	Tyr	Ser	Lys	Phe	Ser	Thr	Gly	Ser	Val	Ser	Ile	Pro	Trp	Gln	
			500					505					510			
aac	gag	atg	ata	gaa	aca	gaa	tgc	ttt	aag	gag	ctg	aac	gtg	ttt	gga	1584
Asn	Glu	Met	Ile	Glu	Thr	Glu	Cys	Phe	Lys	Glu	Leu	Asn	Val	Phe	Gly	
		515					520					525				
cct	aat	ggt	acc	ctc	ccg	cca	gat	ctg	aac	aga	aac	cac	cct	ccg	gaa	1632
Pro	Asn	Gly	Thr	Leu	Pro	Pro	Asp	Leu	Asn	Arg	Asn	His	Pro	Pro	Glu	
		530				535					540					
ccg	ccc	aag	aaa	ggg	ctg	ctc	cag	aga	ctc	ttc	aag	cgg	cag	cat	cag	1680
Pro	Pro	Lys	Lys	Gly	Leu	Leu	Gln	Arg	Leu	Phe	Lys	Arg	Gln	His	Gln	
				545	550				555						560	
aac	aat	tcc	aag	agt	tcg	ccc	agc	tcc	aag	acc	agt	ttt	aac	cac	cac	1728
Asn	Asn	Ser	Lys	Ser	Ser	Pro	Ser	Ser	Lys	Thr	Ser	Phe	Asn	His	His	
			565						570				575			
ata	aac	tca	aac	cat	gtc	agc	tcg	aac	tcc	acc	gga	agc	agc	agg	gat	1776
Ile	Asn	Ser	Asn	His	Val	Ser	Ser	Asn	Ser	Thr	Gly	Ser	Ser	Arg	Asp	
			580					585					590			
cca	ccg	gtc	gcc	acc	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	1824
Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	
		595				600						605				
gtg	gtg	ccc	atc	ctg	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	1872
Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	
		610			615						620					
ttc	agc	gtg	tcc	ggc	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	1920
Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	
				625	630				635						640	
acc	ctg	aag	ttc	atc	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	1968
Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	
			645						650					655		
acc	ctc	gtg	acc	acc	ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	2016
Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	
			660					665					670			
ccc	gac	cac	atg	aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	2064
Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	
		675					680					685				
ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	2112
Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	
		690			695						700					
aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	2160
Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	
		705		710					715					720		
atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	2208
Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	
			725					730						735		
cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	Asn	Val	Tyr	atc	atg	gcc	2256
His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn			Ile	Met	Ala	
			740				745						750			
gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	2304
Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	
		755					760					765				
atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	2352
Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	
		770			775						780					
ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	2400
Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	
				785	790				795						800	
acc	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	2448
Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	

gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	2496
Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	
			820						825				830			
gag	ctg	tac	aag	taa												2511
Glu	Leu	Tyr	Lys													
			835													

<210> 61

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Grk5-EGFP fusion

<400> 61

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Glu	Gly	Gly	Gly	Gly	Lys	Arg	Lys	Gly	Lys	Ser	Lys	Lys	Trp	Lys	Glu	
			20					25					30			
Ile	Leu	Lys	Phe	Pro	His	Ile	Ser	Gln	Cys	Glu	Asp	Leu	Arg	Arg	Thr	
		35					40				45					
Ile	Asp	Arg	Asp	Tyr	Cys	Ser	Leu	Cys	Asp	Lys	Gln	Pro	Ile	Gly	Arg	
	50				55						60					
Leu	Leu	Phe	Arg	Gln	Phe	Cys	Glu	Thr	Arg	Pro	Gly	Leu	Glu	Cys	Tyr	
65				70					75					80		
Ile	Gln	Phe	Leu	Asp	Ser	Val	Ala	Glu	Tyr	Glu	Val	Thr	Pro	Asp	Glu	
			85					90					95			
Lys	Leu	Gly	Glu	Lys	Gly	Lys	Glu	Ile	Met	Thr	Lys	Tyr	Leu	Thr	Pro	
			100					105					110			
Lys	Ser	Pro	Val	Phe	Ile	Ala	Gln	Val	Gly	Gln	Asp	Leu	Val	Ser	Gln	
		115				120					125					
Thr	Glu	Glu	Lys	Leu	Leu	Gln	Lys	Pro	Cys	Lys	Glu	Leu	Phe	Ser	Ala	
	130					135					140					
Cys	Ala	Gln	Ser	Val	His	Glu	Tyr	Leu	Arg	Gly	Glu	Pro	Phe	His	Glu	
145				150						155					160	
Tyr	Leu	Asp	Ser	Met	Phe	Phe	Asp	Arg	Phe	Leu	Gln	Trp	Lys	Trp	Leu	
			165						170					175		
Glu	Arg	Gln	Pro	Val	Thr	Lys	Asn	Thr	Phe	Arg	Gln	Tyr	Arg	Val	Leu	
			180				185						190			
Gly	Lys	Gly	Gly	Phe	Gly	Glu	Val	Cys	Ala	Cys	Gln	Val	Arg	Ala	Thr	
		195					200					205				
Gly	Lys	Met	Tyr	Ala	Cys	Lys	Arg	Leu	Glu	Lys	Lys	Arg	Ile	Lys	Lys	
	210				215						220					
Arg	Lys	Gly	Glu	Ser	Met	Ala	Leu	Asn	Glu	Lys	Gln	Ile	Leu	Glu	Lys	
225				230						235				240		
Val	Asn	Ser	Gln	Phe	Val	Val	Asn	Leu	Ala	Tyr	Ala	Tyr	Glu	Thr	Lys	
			245						250					255		
Asp	Ala	Leu	Cys	Leu	Val	Leu	Thr	Ile	Met	Asn	Gly	Gly	Asp	Leu	Lys	
		260					265						270			
Phe	His	Ile	Tyr	Asn	Met	Gly	Asn	Pro	Gly	Phe	Glu	Glu	Glu	Arg	Ala	
	275					280						285				
Leu	Phe	Tyr	Ala	Ala	Glu	Ile	Leu	Cys	Gly	Leu	Glu	Asp	Leu	His	Arg	
	290				295						300					
Glu	Asn	Thr	Val	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Ile	Leu	Leu	Asp	

305					310					315				320
Asp	Tyr	Gly	His	Ile	Arg	Ile	Ser	Asp	Leu	Gly	Leu	Ala	Val	Lys Ile
				325					330					335
Pro	Glu	Gly	Asp	Leu	Ile	Arg	Gly	Arg	Val	Gly	Thr	Val	Gly	Tyr Met
			340					345					350	
Ala	Pro	Glu	Val	Leu	Asn	Asn	Gln	Arg	Tyr	Gly	Leu	Ser	Pro	Asp Tyr
		355					360				365			
Trp	Gly	Leu	Gly	Cys	Leu	Ile	Tyr	Glu	Met	Ile	Glu	Gly	Gln	Ser Pro
	370					375					380			
Phe	Arg	Gly	Arg	Lys	Glu	Lys	Val	Lys	Arg	Glu	Glu	Val	Asp	Arg Arg
385					390					395				400
Val	Leu	Glu	Thr	Glu	Glu	Val	Tyr	Ser	His	Lys	Phe	Ser	Glu	Glu Ala
			405						410					415
Lys	Ser	Ile	Cys	Lys	Met	Leu	Leu	Thr	Lys	Asp	Ala	Lys	Gln	Arg Leu
			420					425					430	
Gly	Cys	Gln	Glu	Glu	Gly	Ala	Ala	Glu	Val	Lys	Arg	His	Pro	Phe Phe
		435				440						445		
Arg	Asn	Met	Asn	Phe	Lys	Arg	Leu	Glu	Ala	Gly	Met	Leu	Asp	Pro Pro
	450					455					460			
Phe	Val	Pro	Asp	Pro	Arg	Ala	Val	Tyr	Cys	Lys	Asp	Val	Leu	Asp Ile
465					470					475				480
Glu	Gln	Phe	Ser	Thr	Val	Lys	Gly	Val	Asn	Leu	Asp	His	Thr	Asp Asp
			485					490						495
Asp	Phe	Tyr	Ser	Lys	Phe	Ser	Thr	Gly	Ser	Val	Ser	Ile	Pro	Trp Gln
		500						505					510	
Asn	Glu	Met	Ile	Glu	Thr	Glu	Cys	Phe	Lys	Glu	Leu	Asn	Val	Phe Gly
	515					520						525		
Pro	Asn	Gly	Thr	Leu	Pro	Pro	Asp	Leu	Asn	Arg	Asn	His	Pro	Pro Glu
	530					535					540			
Pro	Pro	Lys	Lys	Gly	Leu	Leu	Gln	Arg	Leu	Phe	Lys	Arg	Gln	His Gln
545					550					555				560
Asn	Asn	Ser	Lys	Ser	Ser	Pro	Ser	Ser	Lys	Thr	Ser	Phe	Asn	His His
			565						570					575
Ile	Asn	Ser	Asn	His	Val	Ser	Ser	Asn	Ser	Thr	Gly	Ser	Ser	Arg Asp
		580						585					590	
Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr Gly
		595				600						605		
Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His Lys
	610					615					620			
Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys Leu
625					630					635				640
Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp Pro
			645					650						655
Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg Tyr
		660						665					670	
Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro Glu
		675					680					685		
Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn Tyr
	690				695						700			
Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn Arg
705					710					715				720
Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu Gly
			725						730					735
His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met Ala
		740					745						750	
Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His Asn
	755					760						765		
Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn Thr
	770					775					780			
Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu Ser
785					790				795					800
Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His Met
				805					810					815

Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp  
820 825 830  
Glu Leu Tyr Lys  
835

<210> 62

<211> 1893

<212> DNA

<213> Artificial Sequence

<220>

<223> Jnk1-EGFP Fusion

<220>

<221> CDS

<222> (1)..(1890)

<400> 62

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gat tct aca ttc aca gtc ctg aaa cga tat cag aat tta aaa cct ata	96
Asp Ser Thr Phe Thr Val Leu Lys Arg Tyr Gln Asn Leu Lys Pro Ile	
20 25 30	
ggc tca gga gct caa gga ata gta tgc gca gct tat gat gcc att ctt	144
Gly Ser Gly Ala Gln Gly Ile Val Cys Ala Ala Tyr Asp Ala Ile Leu	
35 40 45	
gaa aga aat gtt gca atc aag aag cta agc cga cca ttt cag aat cag	192
Glu Arg Asn Val Ala Ile Lys Lys Leu Ser Arg Pro Phe Gln Asn Gln	
50 55 60	
act cat gcc aag cgg gcc tac aga gag cta gtt ctt atg aaa tgt gtt	240
Thr His Ala Lys Arg Ala Tyr Arg Glu Leu Val Leu Met Lys Cys Val	
65 70 75 80	
aat cac aaa aat ata att ggc ctt ttg aat gtt ttc aca cca cag aaa	288
Asn His Lys Asn Ile Gly Leu Leu Asn Val Phe Thr Pro Gln Lys	
85 90 95	
tcc cta gaa gaa ttt caa gat gtt tac ata gtc atg gag ctc atg gat	336
Ser Leu Glu Glu Phe Gln Asp Val Tyr Ile Val Met Glu Leu Met Asp	
100 105 110	
gca aat ctt tgc caa gtg att cag atg gag cta gat cat gaa aga atg	384
Ala Asn Leu Cys Gln Val Ile Gln Met Glu Leu Asp His Glu Arg Met	
115 120 125	
tcc tac ctt ctc tat cag atg ctg tgt gga atc aag cac ctt cat tct	432
Ser Tyr Leu Leu Tyr Gln Met Leu Cys Gly Ile Lys His Leu His Ser	
130 135 140	
gct gga att att cat cgg gac tta aag ccc agt aat ata gta gta aaa	480
Ala Gly Ile Ile His Arg Asp Leu Lys Pro Ser Asn Ile Val Val Lys	
145 150 155 160	
tct gat tgc act ttg aag att ctt gac ttc ggt ctg gcc agg act gca	528
Ser Asp Cys Thr Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg Thr Ala	
165 170 175	
gga acg agt ttt atg atg acg cct tat gta gtg act cgc tac tac aga	576

Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg	
			180					185					190			
gca	ccc	gag	gtc	atc	ctt	ggc	atg	ggc	tac	aag	gaa	aac	gtg	gat	tta	624
Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Leu	
		195					200					205				
tgg	tct	gtg	ggg	tgc	att	atg	gga	gaa	atg	gtt	tgc	cac	aaa	atc	ctc	672
Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met	Val	Cys	His	Lys	Ile	Leu	
	210					215					220					
ttt	cca	gga	agg	gac	tat	att	gat	cag	tgg	aat	aaa	gtt	att	gaa	cag	720
Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln	
225					230					235					240	
ctt	gga	aca	cca	tgt	cct	gaa	ttc	atg	aag	aaa	ctg	caa	cca	aca	gta	768
Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val	
				245					250					255		
agg	act	tac	gtt	gaa	aac	aga	cct	aaa	tat	gct	gga	tat	agc	ttt	gag	816
Arg	Thr	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Ala	Gly	Tyr	Ser	Phe	Glu	
			260				265						270			
aaa	ctc	ttc	cct	gat	gtc	ctt	ttc	cca	gct	gac	tca	gaa	cac	aac	aaa	864
Lys	Leu	Phe	Pro	Asp	Val	Leu	Phe	Pro	Ala	Asp	Ser	Glu	His	Asn	Lys	
		275					280					285				
ctt	aaa	gcc	agt	cag	gca	agg	gat	ttg	tta	tcc	aaa	atg	ctg	gta	ata	912
Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile	
	290					295					300					
gat	gca	tct	aaa	agg	atc	tct	gta	gat	gaa	gct	ctc	caa	cac	ccg	tac	960
Asp	Ala	Ser	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Gln	His	Pro	Tyr	
305					310					315					320	
atc	aat	gtc	tgg	tat	gat	cct	tct	gaa	gca	gaa	gct	cca	cca	cca	aag	1008
Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ser	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Lys	
				325					330					335		
atc	cct	gac	aag	cag	tta	gat	gaa	agg	gaa	cac	aca	ata	gaa	gag	tgg	1056
Ile	Pro	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu	His	Thr	Ile	Glu	Glu	Trp	
			340				345						350			
aaa	gaa	ttg	ata	tat	aag	gaa	gtt	atg	gac	ttg	gag	gag	aga	acc	aag	1104
Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Leu	Glu	Glu	Arg	Thr	Lys	
		355					360					365				
aat	gga	gtt	ata	cgg	ggg	cag	ccc	tct	cct	tta	gca	cag	gtg	cag	cag	1152
Asn	Gly	Val	Ile	Arg	Gly	Gln	Pro	Ser	Pro	Leu	Ala	Gln	Val	Gln	Gln	
	370					375					380					
tgg	gat	cca	ccg	gtc	gcc	acc	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	1200
Trp	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	
385					390					395					400	
acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	1248
Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	
				405					410					415		
cac	aag	ttc	agc	gtg	tcc	ggc	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	1296
His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	
			420					425					430			
aag	ctg	acc	ctg	aag	ttc	atc	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	1344
Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	
		435					440					445				
tgg	ccc	acc	ctc	gtg	acc	acc	ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	1392
Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	
	450					455					460					
cgc	tac	ccc	gac	cac	atg	aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	1440
Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	
465					470					475					480	
ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	1488
Pro	Glu	Gly	Tyr	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Gly	
				485					490					495		
aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	1536
Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	
			500					505					510			
aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	1584

Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile		
		515					520					525					
ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	tat	atc	1632	
Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile		
		530					535					540					
atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	1680	
Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg		
545					550					555					560		
cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	1728	
His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln		
				565					570					575			
aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	1776	
Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr		
			580					585					590				
ctg	agc	acc	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	1824	
Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp		
		595					600					605					
cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	1872	
His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly		
	610					615					620						
atg	gac	gag	ctg	tac	aag	taa										1893	
Met	Asp	Glu	Leu	Tyr	Lys												
625					630												

<210> 63

<211> 630

<212> PRT

<213> Artificial Sequence

<220>

<223> Jnk1-EGFP Fusion

<400> 63

Met	Ser	Arg	Ser	Lys	Arg	Asp	Asn	Asn	Phe	Tyr	Ser	Val	Glu	Ile	Gly		
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Asp	Ser	Thr	Phe	Thr	Val	Leu	Lys	Arg	Tyr	Gln	Asn	Leu	Lys	Pro	Ile		
			20					25					30				
Gly	Ser	Gly	Ala	Gln	Gly	Ile	Val	Cys	Ala	Ala	Tyr	Asp	Ala	Ile	Leu		
		35				40						45					
Glu	Arg	Asn	Val	Ala	Ile	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Asn	Gln		
		50				55					60						
Thr	His	Ala	Lys	Arg	Ala	Tyr	Arg	Glu	Leu	Val	Leu	Met	Lys	Cys	Val		
65				70					75					80			
Asn	His	Lys	Asn	Ile	Ile	Gly	Leu	Leu	Asn	Val	Phe	Thr	Pro	Gln	Lys		
			85						90					95			
Ser	Leu	Glu	Glu	Phe	Gln	Asp	Val	Tyr	Ile	Val	Met	Glu	Leu	Met	Asp		
			100					105					110				
Ala	Asn	Leu	Cys	Gln	Val	Ile	Gln	Met	Glu	Leu	Asp	His	Glu	Arg	Met		
		115					120					125					
Ser	Tyr	Leu	Leu	Tyr	Gln	Met	Leu	Cys	Gly	Ile	Lys	His	Leu	His	Ser		
		130				135					140						
Ala	Gly	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Ile	Val	Val	Lys		
145				150					155					160			
Ser	Asp	Cys	Thr	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	Thr	Ala		
				165					170					175			

Gly	Thr	Ser	Phe	Met	Met	Thr	Pro	Tyr	Val	Val	Thr	Arg	Tyr	Tyr	Arg			
			180					185					190					
Ala	Pro	Glu	Val	Ile	Leu	Gly	Met	Gly	Tyr	Lys	Glu	Asn	Val	Asp	Leu			
		195					200					205						
Trp	Ser	Val	Gly	Cys	Ile	Met	Gly	Glu	Met	Val	Cys	His	Lys	Ile	Leu			
	210					215					220							
Phe	Pro	Gly	Arg	Asp	Tyr	Ile	Asp	Gln	Trp	Asn	Lys	Val	Ile	Glu	Gln			
225					230					235					240			
Leu	Gly	Thr	Pro	Cys	Pro	Glu	Phe	Met	Lys	Lys	Leu	Gln	Pro	Thr	Val			
				245					250					255				
Arg	Thr	Tyr	Val	Glu	Asn	Arg	Pro	Lys	Tyr	Ala	Gly	Tyr	Ser	Phe	Glu			
			260					265					270					
Lys	Leu	Phe	Pro	Asp	Val	Leu	Phe	Pro	Ala	Asp	Ser	Glu	His	Asn	Lys			
		275					280					285						
Leu	Lys	Ala	Ser	Gln	Ala	Arg	Asp	Leu	Leu	Ser	Lys	Met	Leu	Val	Ile			
	290					295					300							
Asp	Ala	Ser	Lys	Arg	Ile	Ser	Val	Asp	Glu	Ala	Leu	Gln	His	Pro	Tyr			
305					310					315					320			
Ile	Asn	Val	Trp	Tyr	Asp	Pro	Ser	Glu	Ala	Glu	Ala	Pro	Pro	Pro	Lys			
				325					330						335			
Ile	Pro	Asp	Lys	Gln	Leu	Asp	Glu	Arg	Glu	His	Thr	Ile	Glu	Glu	Trp			
			340				345						350					
Lys	Glu	Leu	Ile	Tyr	Lys	Glu	Val	Met	Asp	Leu	Glu	Glu	Arg	Thr	Lys			
		355					360					365						
Asn	Gly	Val	Ile	Arg	Gly	Gln	Pro	Ser	Pro	Leu	Ala	Gln	Val	Gln	Gln			
	370					375					380							
Trp	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe			
385					390					395					400			
Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly			
				405					410					415				
His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly			
			420				425						430					
Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro			
		435					440					445						
Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser			
	450					455					460							
Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met			
465					470					475					480			
Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly			
				485					490					495				
Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val			
			500					505					510					
Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile			
		515					520					525						
Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile			
	530					535					540							
Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg			
545					550					555					560			
His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln			
				565					570					575				
Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr			
			580				585						590					
Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp			
		595					600					605						
His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly			
	610					615					620							
Met	Asp	Glu	Leu	Tyr	Lys													
625					630													

<210> 64



<211> 1821  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> p38-EGFP fusion

<220>

<221> CDS

<222> (1)..(1818)

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atc tgg gag gtg ccc gag cgt tac cag aac ctg tct cca gtg ggc tct      96
Ile Trp Glu Val Pro Glu Arg Tyr Gln Asn Leu Ser Pro Val Gly Ser
20      25      30
ggc gcc tat ggc tct gtg tgt gct gct ttt gac aca aaa acg ggg tta      144
Gly Ala Tyr Gly Ser Val Cys Ala Ala Phe Asp Thr Lys Thr Gly Leu
35      40      45
cgt gtg gca gtg aag aag ctc tcc aga cca ttt cag tcc atc att cat      192
Arg Val Ala Val Lys Lys Leu Ser Arg Pro Phe Gln Ser Ile Ile His
50      55      60
gcg aaa aga acc tac aga gaa ctg cgg tta ctt aaa cat atg aaa cat      240
Ala Lys Arg Thr Tyr Arg Glu Leu Arg Leu Leu Lys His Met Lys His
65      70      75      80
gaa aat gtg att ggt ctg ttg gac gtt ttt aca cct gca agg tct ctg      288
Glu Asn Val Ile Gly Leu Leu Asp Val Phe Thr Pro Ala Arg Ser Leu
85      90      95
gag gaa ttc aat gat gtg tat ctg gtg acc cat ctc atg ggg gca gat      336
Glu Glu Phe Asn Asp Val Tyr Leu Val Thr His Leu Met Gly Ala Asp
100      105      110
ctg aac aac att gtg aaa tgt cag aag ctt aca gat gac cat gtt cag      384
Leu Asn Asn Ile Val Lys Cys Gln Lys Leu Thr Asp Asp His Val Gln
115      120      125
ttc ctt atc tac caa att ctc cga ggt cta aag tat ata cat tca gct      432
Phe Leu Ile Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala
130      135      140
gac ata att cac agg gac cta aaa cct agt aat cta gct gtg aat gaa      480
Asp Ile Ile His Arg Asp Leu Lys Pro Ser Asn Leu Ala Val Asn Glu
145      150      155      160
gac tgt gag ctg aag att ctg gat ttt gga ctg gct cgg cac aca gat      528
Asp Cys Glu Leu Lys Ile Leu Asp Phe Gly Leu Ala Arg His Thr Asp
165      170      175
gat gaa atg aca ggc tac gtg gcc act agg tgg tac agg gct cct gag      576
Asp Glu Met Thr Gly Tyr Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu
180      185      190
atc atg ctg aac tgg atg cat tac aac cag aca gtt gat att tgg tca      624
Ile Met Leu Asn Trp Met His Tyr Asn Gln Thr Val Asp Ile Trp Ser
195      200      205
gtg gga tgc ata atg gcc gag ctg ttg act gga aga aca ttg ttt cct      672
Val Gly Cys Ile Met Ala Glu Leu Leu Thr Gly Arg Thr Leu Phe Pro
210      215      220

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ggt aca gac cat att gat cag ttg aag ctc att tta aga ctc gtt gga	720
Gly Thr Asp His Ile Asp Gln Leu Lys Leu Ile Leu Arg Leu Val Gly	
225 230 235 240	
acc cca ggg gct gag ctt ttg aag aaa atc tcc tca gag tct gca aga	768
Thr Pro Gly Ala Glu Leu Leu Lys Lys Ile Ser Ser Glu Ser Ala Arg	
245 250 255	
aac tat att cag tct ttg act cag atg ccg aag atg aac ttt gcg aat	816
Asn Tyr Ile Gln Ser Leu Thr Gln Met Pro Lys Met Asn Phe Ala Asn	
260 265 270	
gta ttt att ggt gcc aat ccc ctg gct gtc gac ttg ctg gag aag atg	864
Val Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met	
275 280 285	
ctt gta ttg gac tca gat aag aga att aca gcg gcc caa gcc ctt gca	912
Leu Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala	
290 295 300	
cat gcc tac ttt gct cag tac cac gat cct gat gat gaa cca gtg gcc	960
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala	
305 310 315 320	
gat cct tat gat cag tcc ttt gaa agc agg gac ctc ctt ata gat gag	1008
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu	
325 330 335	
tgg aaa agc ctg acc tat gat gaa gtc atc agc ttt gtg cca cca ccc	1056
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro	
340 345 350	
ctt gac caa gaa gag atg gag tcc gag gat cca ccg gtc gcc acc atg	1104
Leu Asp Gln Glu Glu Met Glu Ser Glu Asp Pro Pro Val Ala Thr Met	
355 360 365	
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	1152
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
370 375 380	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	1200
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
385 390 395 400	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	1248
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
405 410 415	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	1296
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
420 425 430	
acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag	1344
Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
435 440 445	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	1392
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
450 455 460	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	1440
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
465 470 475 480	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	1488
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
485 490 495	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	1536
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
500 505 510	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	1584
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
515 520 525	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	1632
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
530 535 540	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc	1680
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	
545 550 555 560	

gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	agc	1728
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	
			565						570					575		
aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	1776
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	
			580					585					590			
acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	taa		1821
Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys			
		595					600					605				

<210> 65

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> p38-EGFP fusion

<400> 65

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Ile	Trp	Glu	Val	Pro	Glu	Arg	Tyr	Gln	Asn	Leu	Ser	Pro	Val	Gly	Ser	
			20					25					30			
Gly	Ala	Tyr	Gly	Ser	Val	Cys	Ala	Ala	Phe	Asp	Thr	Lys	Thr	Gly	Leu	
		35					40					45				
Arg	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Ile	Ile	His	
	50					55					60					
Ala	Lys	Arg	Thr	Tyr	Arg	Glu	Leu	Arg	Leu	Leu	Lys	His	Met	Lys	His	
65				70					75					80		
Glu	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Arg	Ser	Leu	
			85					90					95			
Glu	Glu	Phe	Asn	Asp	Val	Tyr	Leu	Val	Thr	His	Leu	Met	Gly	Ala	Asp	
			100					105					110			
Leu	Asn	Asn	Ile	Val	Lys	Cys	Gln	Lys	Leu	Thr	Asp	Asp	His	Val	Gln	
		115					120					125				
Phe	Leu	Ile	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	
	130					135					140					
Asp	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Ala	Val	Asn	Glu	
145				150					155					160		
Asp	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	His	Thr	Asp	
			165					170						175		
Asp	Glu	Met	Thr	Gly	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	
			180					185					190			
Ile	Met	Leu	Asn	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser	
		195				200						205				
Val	Gly	Cys	Ile	Met	Ala	Glu	Leu	Leu	Thr	Gly	Arg	Thr	Leu	Phe	Pro	
	210				215						220					
Gly	Thr	Asp	His	Ile	Asp	Gln	Leu	Lys	Leu	Ile	Leu	Arg	Leu	Val	Gly	
225				230					235					240		
Thr	Pro	Gly	Ala	Glu	Leu	Leu	Lys	Lys	Ile	Ser	Ser	Glu	Ser	Ala	Arg	
			245						250					255		
Asn	Tyr	Ile	Gln	Ser	Leu	Thr	Gln	Met	Pro	Lys	Met	Asn	Phe	Ala	Asn	
		260						265					270			
Val	Phe	Ile	Gly	Ala	Asn	Pro	Leu	Ala	Val	Asp	Leu	Leu	Glu	Lys	Met	
		275				280						285				
Leu	Val	Leu	Asp	Ser	Asp	Lys	Arg	Ile	Thr	Ala	Ala	Gln	Ala	Leu	Ala	

290	295	300
His Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala		
305	310	315
Asp Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu		320
	325	330
Trp Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Pro		335
	340	345
Leu Asp Gln Glu Glu Met Glu Ser Glu Asp Pro Pro Val Ala Thr Met		350
	355	360
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		365
	370	375
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		380
385	390	395
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		400
	405	410
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		415
	420	425
Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln		430
	435	440
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		445
	450	455
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		460
465	470	475
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		480
	485	490
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		495
	500	505
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		510
	515	520
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		525
	530	535
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		540
545	550	555
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		560
	565	570
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		575
	580	585
Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys		590
	595	600

<210> 66

<211> 2913

<212> DNA

<213> Artificial Sequence

<220>

<223> p85alpha-EGFP fusion

<220>

<221> CDS

<222> (1)..(2910)





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Asn	Lys	Thr	Ala	Thr	Gly	Tyr	Gly	Phe	Ala	Glu	Pro	Tyr	Asn	Leu	Tyr	
		675					680					685				
agc	tct	ctg	aaa	gaa	ctg	gtg	cta	cat	tac	caa	cac	acc	tcc	ctt	gtg	2112
Ser	Ser	Leu	Lys	Glu	Leu	Val	Leu	His	Tyr	Gln	His	Thr	Ser	Leu	Val	
		690				695					700					
cag	cac	aac	gac	tcc	ctc	aat	gtc	aca	cta	gcc	tac	cca	gta	tat	gca	2160
Gln	His	Asn	Asp	Ser	Leu	Asn	Val	Thr	Leu	Ala	Tyr	Pro	Val	Tyr	Ala	
		705			710					715					720	
cag	cag	agg	cga	cag	gat	cca	ccg	gtc	gcc	acc	atg	gtg	agc	aag	ggc	2208
Gln	Gln	Arg	Arg	Gln	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	
			725						730					735		
gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	gag	ctg	gac	ggc	2256
Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	
			740					745					750			
gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	ggc	gag	ggc	gat	2304
Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	
		755				760				765						
gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	acc	ggc	aag		2352
Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	
		770			775						780					
ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg	acc	tac	ggc	gtg	2400
Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	
				790					795					800		
cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	cag	cac	gac	ttc	ttc	2448
Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	
			805						810					815		
aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	ttc	2496
Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	
		820						825					830			
aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	ggc	2544
Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	
		835				840						845				
gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	gag	2592
Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	
		850			855					860						
gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	2640
Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	
		865		870						875					880	
aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	2688
Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	
			885					890						895		
ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	ggc	gac	2736
Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	
		900					905						910			
cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	2784
His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	
		915				920						925				
gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	2832
Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	
		930			935						940					
gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	2880
Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	
		945			950					955					960	
atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	taa						2913
Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys							
			965						970							

<210> 67

<211> 970

<212> PRT

<213> Artificial Sequence

<220>

<223> p85alpha-EGFP fusion

<400> 67

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20     25     30
Asn Lys Gly Ser Leu Val Ala Leu Gly Phe Ser Asp Gly Gln Glu Ala
35     40     45
Arg Pro Glu Glu Ile Gly Trp Leu Asn Gly Tyr Asn Glu Thr Thr Gly
50     55     60
Glu Arg Gly Asp Phe Pro Gly Thr Tyr Val Glu Tyr Ile Gly Arg Lys
65     70     75     80
Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro
85     90     95
Val Ala Pro Gly Ser Ser Lys Thr Glu Ala Asp Val Glu Gln Gln Ala
100    105    110
Leu Thr Leu Pro Asp Leu Ala Glu Gln Phe Ala Pro Pro Asp Ile Ala
115    120    125
Pro Pro Leu Leu Ile Lys Leu Val Glu Ala Ile Glu Lys Lys Gly Leu
130    135    140
Glu Cys Ser Thr Leu Tyr Arg Thr Gln Ser Ser Asn Leu Ala Glu
145    150    155    160
Leu Arg Gln Leu Leu Asp Cys Asp Thr Pro Ser Val Asp Leu Glu Met
165    170    175
Ile Asp Val His Val Leu Ala Asp Ala Phe Lys Arg Tyr Leu Leu Asp
180    185    190
Leu Pro Asn Pro Val Ile Pro Ala Ala Val Tyr Ser Glu Met Ile Ser
195    200    205
Leu Ala Pro Glu Val Gln Ser Ser Glu Glu Tyr Ile Gln Leu Leu Lys
210    215    220
Lys Leu Ile Arg Ser Pro Ser Ile Pro His Gln Tyr Trp Leu Thr Leu
225    230    235    240
Gln Tyr Leu Leu Lys His Phe Phe Lys Leu Ser Gln Thr Ser Ser Lys
245    250    255
Asn Leu Leu Asn Ala Arg Val Leu Ser Glu Ile Phe Ser Pro Met Leu
260    265    270
Phe Arg Phe Ser Ala Ala Ser Ser Asp Asn Thr Glu Asn Leu Ile Lys
275    280    285
Val Ile Glu Ile Leu Ile Ser Thr Glu Trp Asn Glu Arg Gln Pro Ala
290    295    300
Pro Ala Leu Pro Pro Lys Pro Pro Lys Pro Thr Thr Val Ala Asn Asn
305    310    315    320
Gly Met Asn Asn Asn Met Ser Leu Gln Asn Ala Glu Trp Tyr Trp Gly
325    330    335
Asp Ile Ser Arg Glu Glu Val Asn Glu Lys Leu Arg Asp Thr Ala Asp
340    345    350
Gly Thr Phe Leu Val Arg Asp Ala Ser Thr Lys Met His Gly Asp Tyr
355    360    365
Thr Leu Thr Leu Arg Lys Gly Gly Asn Asn Lys Leu Ile Lys Ile Phe
370    375    380
His Arg Asp Gly Lys Tyr Gly Phe Ser Asp Pro Leu Thr Phe Ser Ser
385    390    395    400
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Val Val Glu Leu Ile Asn His Tyr Arg Asn Glu Ser Leu Ala Gln Tyr  
405 410 415  
Asn Pro Lys Leu Asp Val Lys Leu Leu Tyr Pro Val Ser Lys Tyr Gln  
420 425 430  
Gln Asp Gln Val Val Lys Glu Asp Asn Ile Glu Ala Val Gly Lys Lys  
435 440 445  
Leu His Glu Tyr Asn Thr Gln Phe Gln Glu Lys Ser Arg Glu Tyr Asp  
450 455 460  
Arg Leu Tyr Glu Glu Tyr Thr Arg Thr Ser Gln Glu Ile Gln Met Lys  
465 470 475 480  
Arg Thr Ala Ile Glu Ala Phe Asn Glu Thr Ile Lys Ile Phe Glu Glu  
485 490 495  
Gln Cys Gln Thr Gln Glu Arg Tyr Ser Lys Glu Tyr Ile Glu Lys Phe  
500 505 510  
Lys Arg Glu Gly Asn Glu Lys Glu Ile Gln Arg Ile Met His Asn Tyr  
515 520 525  
Asp Lys Leu Lys Ser Arg Ile Ser Glu Ile Ile Asp Ser Arg Arg Arg  
530 535 540  
Leu Glu Glu Asp Leu Lys Lys Gln Ala Ala Glu Tyr Arg Glu Ile Asp  
545 550 555 560  
Lys Arg Met Asn Ser Ile Lys Pro Asp Leu Ile Gln Leu Arg Lys Thr  
565 570 575  
Arg Asp Gln Tyr Leu Met Trp Leu Thr Gln Lys Gly Val Arg Gln Lys  
580 585 590  
Lys Leu Asn Glu Trp Leu Gly Asn Glu Asn Thr Glu Asp Gln Tyr Ser  
595 600 605  
Leu Val Glu Asp Asp Glu Asp Leu Pro His His Asp Glu Lys Thr Trp  
610 615 620  
Asn Val Gly Ser Ser Asn Arg Asn Lys Ala Glu Asn Leu Leu Arg Gly  
625 630 635 640  
Lys Arg Asp Gly Thr Phe Leu Val Arg Glu Ser Ser Lys Gln Gly Cys  
645 650 655  
Tyr Ala Cys Ser Val Val Val Asp Gly Glu Val Lys His Cys Val Ile  
660 665 670  
Asn Lys Thr Ala Thr Gly Tyr Gly Phe Ala Glu Pro Tyr Asn Leu Tyr  
675 680 685  
Ser Ser Leu Lys Glu Leu Val Leu His Tyr Gln His Thr Ser Leu Val  
690 695 700  
Gln His Asn Asp Ser Leu Asn Val Thr Leu Ala Tyr Pro Val Tyr Ala  
705 710 715 720  
Gln Gln Arg Arg Gln Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly  
725 730 735  
Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly  
740 745 750  
Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp  
755 760 765  
Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys  
770 775 780  
Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val  
785 790 795 800  
Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe  
805 810 815  
Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe  
820 825 830  
Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly  
835 840 845  
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu  
850 855 860  
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His  
865 870 875 880  
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn  
885 890 895  
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp



145	150	155	160	
ctg gac ctc atc tac cgg gac ctg aag ccc gag aat ctt ctc atc gac				528
Leu Asp Leu Ile Tyr Arg Asp Leu Lys Pro Glu Asn Leu Leu Ile Asp				
	165	170	175	
cag cag ggc tat att cag gtg aca gac ttc ggt ttt gcc aag cgt gtg				576
Gln Gln Gly Tyr Ile Gln Val Thr Asp Phe Gly Phe Ala Lys Arg Val				
	180	185	190	
aaa ggc cgt act tgg acc ttg tgt ggg acc cct gag tac ttg gcc ccc				624
Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro				
	195	200	205	
gag att atc ctg agc aaa ggc tac aac aag gct gtg gac tgg tgg gct				672
Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala				
	210	215	220	
ctc gga gtc ctc atc tac gag atg gct gct ggt tac cca ccc ttc ttc				720
Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe				
	225	230	235	
gct gac cag cct atc cag atc tat gag aaa atc gtc tct ggg aag gtg				768
Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val				
	245	250	255	
cgg ttc cca tcc cac ttc agc tct gac ttg aag gac ctg ctg cgg aac				816
Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn				
	260	265	270	
ctt ctg caa gtg gat cta acc aag cgc ttt gga aac ctc aag gac ggg				864
Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asp Gly				
	275	280	285	
gtc aat gac atc aag aac cac aag tgg ttt gcc acg act gac tgg att				912
Val Asn Asp Ile Lys Asn His Lys Trp Phe Ala Thr Thr Asp Trp Ile				
	290	295	300	
gcc atc tat cag aga aag gtg gaa gct ccc ttc ata cca aag ttt aaa				960
Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Lys				
	305	310	315	
ggc cct ggg gac acg agt aac ttt gac gac tat gag gag gaa gag atc				1008
Gly Pro Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Ile				
	325	330	335	
cgg gtc tcc atc aat gag aag tgt ggc aag gag ttt act gag ttt ggg				1056
Arg Val Ser Ile Asn Glu Lys Cys Gly Lys Glu Phe Thr Glu Phe Gly				
	340	345	350	
cgc gcc atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att				1104
Arg Ala Met Ser Lys Gly Glu Glu Phe Thr Gly Val Val Pro Ile				
	355	360	365	
ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt				1152
Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser				
	370	375	380	
gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt				1200
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe				
	385	390	395	
att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act				1248
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr				
	405	410	415	
act ctc act tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg				1296
Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met				
	420	425	430	
aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag				1344
Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln				
	435	440	445	
gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct				1392
Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala				
	450	455	460	
gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa				1440
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys				
	465	470	475	
ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa				1488
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu				

				485				490					495				
tac	aat	tat	aac	tca	cat	aat	gta	tac	atc	atg	gca	gac	aaa	cca	aag		1536
Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Pro	Lys		
			500					505					510				
aat	ggc	atc	aaa	gtt	aac	ttc	aaa	att	aga	cac	aac	att	aaa	gat	gga		1584
Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Lys	Asp	Gly		
		515					520					525					
agc	gtt	caa	tta	gca	gac	cat	tat	caa	caa	aat	act	cca	att	ggc	gat		1632
Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
	530					535					540						
ggc	cct	gtc	ctt	tta	cca	gac	aac	cat	tac	ctg	tcc	acg	caa	tct	gcc		1680
Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala		
545					550				555				560				
ctt	tcc	aaa	gat	ccc	aac	gaa	aag	aga	gat	cac	atg	atc	ctt	ctt	gag		1728
Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Leu	Leu	Glu		
			565					570					575				
ttt	gta	aca	gct	ggg	att	aca	cat	ggc	atg	gat	gaa	cta	tac	aaa			1776
Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
			580				585					590					
cct	cag	gag	taa														1788
Pro	Gln	Glu															
		595															

<210> 69

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion Construct

<400> 69

Met	Gly	Asn	Ala	Ala	Ala	Ala	Lys	Lys	Gly	Ser	Glu	Gln	Glu	Ser	Val		
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Lys	Glu	Phe	Leu	Ala	Lys	Ala	Lys	Glu	Asp	Phe	Leu	Lys	Lys	Trp	Glu		
			20					25					30				
Asp	Pro	Ser	Gln	Asn	Thr	Ala	Gln	Leu	Asp	Gln	Phe	Asp	Arg	Ile	Lys		
		35				40						45					
Thr	Leu	Gly	Thr	Gly	Ser	Phe	Gly	Arg	Val	Met	Leu	Val	Lys	His	Lys		
	50					55					60						
Glu	Ser	Gly	Asn	His	Tyr	Ala	Met	Lys	Ile	Leu	Asp	Lys	Gln	Lys	Val		
65					70				75					80			
Val	Lys	Leu	Lys	Gln	Ile	Glu	His	Thr	Leu	Asn	Glu	Lys	Arg	Ile	Leu		
			85					90					95				
Gln	Ala	Val	Asn	Phe	Pro	Phe	Leu	Val	Lys	Leu	Glu	Phe	Ser	Phe	Lys		
			100					105					110				
Asp	Asn	Ser	Asn	Leu	Tyr	Met	Val	Met	Glu	Tyr	Val	Ala	Gly	Gly	Glu		
		115				120						125					
Met	Phe	Ser	His	Leu	Arg	Arg	Ile	Gly	Arg	Phe	Ser	Glu	Pro	His	Ala		
	130					135					140						
Arg	Phe	Tyr	Ala	Ala	Gln	Ile	Val	Leu	Thr	Phe	Glu	Tyr	Leu	His	Ser		
145					150					155				160			
Leu	Asp	Leu	Ile	Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Ile	Asp		
			165					170						175			
Gln	Gln	Gly	Tyr	Ile	Gln	Val	Thr	Asp	Phe	Gly	Phe	Ala	Lys	Arg	Val		
			180					185					190				

Lys Gly Arg Thr Trp Thr Leu Cys Gly Thr Pro Glu Tyr Leu Ala Pro  
 195 200 205  
 Glu Ile Ile Leu Ser Lys Gly Tyr Asn Lys Ala Val Asp Trp Trp Ala  
 210 220  
 Leu Gly Val Leu Ile Tyr Glu Met Ala Ala Gly Tyr Pro Pro Phe Phe  
 225 230 235 240  
 Ala Asp Gln Pro Ile Gln Ile Tyr Glu Lys Ile Val Ser Gly Lys Val  
 245 250 255  
 Arg Phe Pro Ser His Phe Ser Ser Asp Leu Lys Asp Leu Leu Arg Asn  
 260 265 270  
 Leu Leu Gln Val Asp Leu Thr Lys Arg Phe Gly Asn Leu Lys Asp Gly  
 275 280 285  
 Val Asn Asp Ile Lys Asn His Lys Trp Phe Ala Thr Thr Asp Trp Ile  
 290 295 300  
 Ala Ile Tyr Gln Arg Lys Val Glu Ala Pro Phe Ile Pro Lys Phe Lys  
 305 310 315 320  
 Gly Pro Gly Asp Thr Ser Asn Phe Asp Asp Tyr Glu Glu Glu Glu Ile  
 325 330 335  
 Arg Val Ser Ile Asn Glu Lys Cys Gly Lys Glu Phe Thr Glu Phe Gly  
 340 345 350  
 Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile  
 355 360 365  
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser  
 370 375 380  
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe  
 385 390 395 400  
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr  
 405 410 415  
 Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met  
 420 425 430  
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln  
 435 440 445  
 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala  
 450 455 460  
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys  
 465 470 475 480  
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu  
 485 490 495  
 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys  
 500 505 510  
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly  
 515 520 525  
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp  
 530 535 540  
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala  
 545 550 555 560  
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu  
 565 570 575  
 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
 580 585 590  
 Pro Gln Glu  
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<210> 70

<211> 2181

<212> DNA

<213> Artificial Sequence

<220>

<223> PKB-EGFP fusion

<220>

<221> CDS

<222> (1)..(2178)

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gag tac atc aag acc tgg cgg cca cgc tac ttc ctc ctc aag aat gat      96
Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp
20                               25                               30
ggc acc ttc att ggc tac aag gag cgg ccg cag gat gtg gac caa cgt      144
Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg
35                               40                               45
gag gct ccc ctc aac aac ttc tct gtg gcg cag tgc cag ctg atg aag      192
Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys
50                               55                               60
acg gag cgg ccc cgg ccc aac acc ttc atc atc cgc tgc ctg cag tgg      240
Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp
65                               70                               75                               80
acc act gtc atc gaa cgc acc ttc cat gtg gag act cct gag gag cgg      288
Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg
85                               90                               95
gag gag tgg aca acc gcc atc cag act gtg gct gac ggc ctc aag aag      336
Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys
100                              105                              110
cag gag gag gag gag atg gac ttc cgg tcg ggc tca ccc agt gac aac      384
Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn
115                              120                              125
tca ggg gct gaa gag atg gag gtg tcc ctg gcc aag ccc aag cac cgc      432
Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg
130                              135                              140
gtg acc atg aac gag ttt gag tac ctg aag ctg ctg ggc aag ggc act      480
Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr
145                              150                              155                              160
ttc ggc aag gtg atc ctg gtg aag gag aag gcc aca ggc cgc tac tac      528
Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr
165                              170                              175
gcc atg aag atc ctc aag aag gaa gtc atc gtg gcc aag gac gag gtg      576
Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val
180                              185                              190
gcc cac aca ctc acc gag aac cgc gtc ctg cag aac tcc agg cac ccc      624
Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro
195                              200                              205
ttc ctc aca gcc ctg aag tac tct ttc cag acc cac gac cgc ctc tgc      672
Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys
210                              215                              220
ttt gtc atg gag tac gcc aac ggg ggc gag ctg ttc ttc cac ctg tcc      720
Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser
225                              230                              235                              240
cgg gaa cgt gtg ttc tcc gag gac cgg gcc cgc ttc tat ggc gct gag      768
Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu
245                              250                              255
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att gtg tca gcc ctg gac tac ctg cac tcg gag aag aac gtg gtg tac	816
Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr	
260 265 270	
cgg gac ctc aag ctg gag aac ctc atg ctg gac aag gac ggg cac att	864
Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile	
275 280 285	
aag atc aca gac ttc ggg ctg tgc aag gag ggg atc aag gac ggt gcc	912
Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala	
290 295 300	
acc atg aag acc ttt tgc ggc aca cct gag tac ctg gcc ccc gag gtg	960
Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val	
305 310 315 320	
ctg gag gac aat gac tac ggc cgt gca gtg gac tgg tgg ggg ctg ggc	1008
Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly	
325 330 335	
gtg gtc atg tac gag atg atg tgc ggt cgc ctg ccc ttc tac aac cag	1056
Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln	
340 345 350	
gac cat gag aag ctt ttt gag ctc atc ctc atg gag gag atc cgc ttc	1104
Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe	
355 360 365	
ccg cgc acg ctt ggt ccc gag gcc aag tcc ttg ctt tca ggg ctg ctc	1152
Pro Arg Thr Leu Gly Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu	
370 375 380	
aag aag gac ccc aag cag agg ctt ggc ggg ggc tcc gag gac gcc aag	1200
Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Ser Glu Asp Ala Lys	
385 390 395 400	
gag atc atg cag cat cgc ttc ttt gcc ggt atc gtg tgg cag cac gtg	1248
Glu Ile Met Gln His Arg Phe Phe Ala Gly Ile Val Trp Gln His Val	
405 410 415	
tac gag aag aag ctc agc cca ccc ttc aag ccc cag gtc acg tcg gag	1296
Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser Glu	
420 425 430	
act gac acc agg tat ttt gat gag gag ttc acg gcc cag atg atc acc	1344
Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr	
435 440 445	
atc aca cca cct gac caa gat gac agc atg gag tgt gtg gac agc gag	1392
Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser Glu	
450 455 460	
cgc agg ccc cac ttc ccc cag ttc tcc tac tcg gcc agc agc acg gcc	1440
Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ser Thr Ala	
465 470 475 480	
tcg gat cca ccg gtc gcc acc atg gtg agc aag ggc gag gag ctg ttc	1488
Ser Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe	
485 490 495	
acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc	1536
Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly	
500 505 510	
cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc	1584
His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly	
515 520 525	
aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc	1632
Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro	
530 535 540	
tgg ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag tgc ttc agc	1680
Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser	
545 550 555 560	
cgc tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg	1728
Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met	
565 570 575	
ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc	1776
Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly	
580 585 590	

aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg	1824
Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val	
595 600 605	
aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc	1872
Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile	
610 615 620	
ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat atc	1920
Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile	
625 630 635 640	
atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc	1968
Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg	
645 650 655	
cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag	2016
His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln	
660 665 670	
aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac	2064
Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr	
675 680 685	
ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat	2112
Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp	
690 695 700	
cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggc atc act ctc ggc	2160
His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly	
705 710 715 720	
atg gac gag ctg tac aag taa	2181
Met Asp Glu Leu Tyr Lys	
725	

<210> 71

<211> 726

<212> PRT

<213> Artificial Sequence

<220>

<223> PKB-EGFP fusion

<400> 71

Met Ser Asp Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly	
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Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp	
20 25 30	
Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg	
35 40 45	
Glu Ala Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys	
50 55 60	
Thr Glu Arg Pro Arg Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp	
65 70 75 80	
Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg	
85 90 95	
Glu Glu Trp Thr Thr Ala Ile Gln Thr Val Ala Asp Gly Leu Lys Lys	
100 105 110	
Gln Glu Glu Glu Glu Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn	
115 120 125	
Ser Gly Ala Glu Glu Met Glu Val Ser Leu Ala Lys Pro Lys His Arg	
130 135 140	



Val	Thr	Met	Asn	Glu	Phe	Glu	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	Gly	Thr	145	150	155	160
Phe	Gly	Lys	Val	Ile	Leu	Val	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Tyr	Tyr	165	170		175
Ala	Met	Lys	Ile	Leu	Lys	Lys	Glu	Val	Ile	Val	Ala	Lys	Asp	Glu	Val	180	185		190
Ala	His	Thr	Leu	Thr	Glu	Asn	Arg	Val	Leu	Gln	Asn	Ser	Arg	His	Pro	195	200		205
Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	His	Asp	Arg	Leu	Cys	210	215		220
Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	225	230		235
Arg	Glu	Arg	Val	Phe	Ser	Glu	Asp	Arg	Ala	Arg	Phe	Tyr	Gly	Ala	Glu	245	250		255
Ile	Val	Ser	Ala	Leu	Asp	Tyr	Leu	His	Ser	Glu	Lys	Asn	Val	Val	Tyr	260	265		270
Arg	Asp	Leu	Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	275	280		285
Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Lys	Asp	Gly	Ala	290	295		300
Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	305	310		315
Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	325	330		335
Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	340	345		350
Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Glu	Ile	Arg	Phe	355	360		365
Pro	Arg	Thr	Leu	Gly	Pro	Glu	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu	370	375		380
Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly	Gly	Gly	Ser	Glu	Asp	Ala	Lys	385	390		395
Glu	Ile	Met	Gln	His	Arg	Phe	Phe	Ala	Gly	Ile	Val	Trp	Gln	His	Val	405	410		415
Tyr	Glu	Lys	Lys	Leu	Ser	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	Glu	420	425		430
Thr	Asp	Thr	Arg	Tyr	Phe	Asp	Glu	Glu	Phe	Thr	Ala	Gln	Met	Ile	Thr	435	440		445
Ile	Thr	Pro	Pro	Asp	Gln	Asp	Ser	Met	Glu	Cys	Val	Asp	Ser	Glu		450	455		460
Arg	Arg	Pro	His	Phe	Pro	Gln	Phe	Ser	Tyr	Ser	Ala	Ser	Ser	Thr	Ala	465	470		475
Ser	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	485	490		495
Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	500	505		510
His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	515	520		525
Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	530	535		540
Trp	Pro	Thr	Leu	Val	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser		545	550		555
Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	565	570		575
Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	580	585		590
Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	595	600		605
Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	610	615		620
Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	625	630		635
Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg				

645 650 655  
 His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln  
 660 665 670  
 Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr  
 675 680 685  
 Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp  
 690 695 700  
 His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly  
 705 710 715 720  
 Met Asp Glu Leu Tyr Lys  
 725

<210> 72

<211> 2751

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion construct

<220>

<221> CDS

<222> (1)..(2748)

<400> 72  
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 Met Ala Asp Val Tyr Pro Ala Asn Asp Ser Thr Ala Ser Gln Asp Val  
 1 5 10 15  
 gcc aac cgc ttc gcc cgc aaa ggg gcg ctg agg cag aag aac gtg cat 96  
 Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His  
 20 25 30  
 gag gtg aaa gac cac aaa ttc atc gcc cgc ttc ttc aag caa ccc acc 144  
 Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr  
 35 40 45  
 ttc tgc agc cac tgc acc gac ttc atc tgg ggg ttt ggg aaa caa ggc 192  
 Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly  
 50 55 60  
 ttc cag tgc caa gtt tgc tgt ttt gtg gtt cat aag agg tgc cat gag 240  
 Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu  
 65 70 75 80  
 ttc gtt acg ttc tct tgt ccg ggt gcg gat aag gga cct gac act gac 288  
 Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp  
 85 90 95  
 gac ccc agg agc aag cac aag ttc aaa atc cac aca tac gga agc cct 336  
 Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro  
 100 105 110  
 acc ttc tgt gat cac tgt ggg tcc ctg ctc tat gga ctt atc cac caa 384  
 Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln  
 115 120 125  
 ggg atg aaa tgt gac acc tgc gac atg aat gtt cac aac cag tgt gtg 432  
 Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Asn Gln Cys Val  
 130 135 140

atc aat gac cct agc ctc tgc gga atg gat cac aca gag aag agg ggg	480
Ile Asn Asp Pro Ser Leu Cys Gly Met Asp His Thr Glu Lys Arg Gly	
145 150 155	
cgg att tat ctg aag gct gag gtc act gat gaa aag ctc cac gtc acg	528
Arg Ile Tyr Leu Lys Ala Glu Val Thr Asp Glu Lys Leu His Val Thr	
165 170 175	
gta cga gat gca aaa aat cta atc cct atg gat cca aat ggg ctt tcg	576
Val Arg Asp Ala Lys Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser	
180 185 190	
gat cct tat gtg aag ctg aaa cta atc cct gac ccc aag aat gag agc	624
Asp Pro Tyr Val Lys Leu Lys Leu Ile Pro Asp Pro Lys Asn Glu Ser	
195 200 205	
aaa cag aaa acc aaa acc atc cgc tcc aac ctg aat cct cag tgg aat	672
Lys Gln Lys Thr Lys Thr Ile Arg Ser Asn Leu Asn Pro Gln Trp Asn	
210 215 220	
gag tcc ttc acg ttc aaa tta aaa cct tca gac aaa gac cgg cga ctg	720
Glu Ser Phe Thr Phe Lys Leu Lys Pro Ser Asp Lys Asp Arg Arg Leu	
225 230 235 240	
tct gta gaa atc tgg gac tgg gat cgg acg act cgg aat gac ttc atg	768
Ser Val Glu Ile Trp Asp Trp Asp Arg Thr Thr Arg Asn Asp Phe Met	
245 250 255	
gga tcc ctt tcc ttt ggt gtc tca gag cta atg aag atg ccg gcc agt	816
Gly Ser Leu Ser Phe Gly Val Ser Glu Leu Met Lys Met Pro Ala Ser	
260 265 270	
gga tgg tat aaa gct cac aac caa gaa gag ggc gaa tat tac aac gtg	864
Gly Trp Tyr Lys Ala His Asn Gln Glu Glu Gly Glu Tyr Tyr Asn Val	
275 280 285	
ccc att cca gaa gga gat gaa gaa ggc aac atg gaa ctc agg cag aag	912
Pro Ile Pro Glu Gly Asp Glu Glu Gly Asn Met Glu Leu Arg Gln Lys	
290 295 300	
ttt gag aaa gcc aag cta ggt cct gtt ggt aac aaa gtc atc agc cct	960
Phe Glu Lys Ala Lys Leu Gly Pro Val Gly Asn Lys Val Ile Ser Pro	
305 310 315 320	
tca gaa gac aga aag caa cca tcc aac aac ctg gac aga gtg aaa ctc	1008
Ser Glu Asp Arg Lys Gln Pro Ser Asn Asn Leu Asp Arg Val Lys Leu	
325 330 335	
aca gac ttc aac ttc ctc atg gtg ctg ggg aag ggg agt ttt ggg aag	1056
Thr Asp Phe Asn Phe Leu Met Val Leu Gly Lys Gly Ser Phe Gly Lys	
340 345 350	
gtg atg ctt gct gac agg aag gga acg gag gaa ctg tac gcc atc aag	1104
Val Met Leu Ala Asp Arg Lys Gly Thr Glu Glu Leu Tyr Ala Ile Lys	
355 360 365	
atc ctg aag aag gac gtg gtg atc cag gac gac gac gtg gag tgc acc	1152
Ile Leu Lys Lys Asp Val Val Ile Gln Asp Asp Asp Val Glu Cys Thr	
370 375 380	
atg gtg gag aag cgc gtg ctg gcc ctg ctg gac aag ccg cca ttt ctg	1200
Met Val Glu Lys Arg Val Leu Ala Leu Leu Asp Lys Pro Pro Phe Leu	
385 390 395 400	
aca cag ctg cac tcc tgc ttc cag aca gtg gac cgg ctg tac ttc gtc	1248
Thr Gln Leu His Ser Cys Phe Gln Thr Val Asp Arg Leu Tyr Phe Val	
405 410 415	
atg gaa tac gtc aac ggc ggg gat ctt atg tac cac att cag caa gtc	1296
Met Glu Tyr Val Asn Gly Gly Asp Leu Met Tyr His Ile Gln Gln Val	
420 425 430	
ggg aaa ttt aag gag cca caa gca gta ttc tac gca gcc gag atc tcc	1344
Gly Lys Phe Lys Glu Pro Gln Ala Val Phe Tyr Ala Ala Glu Ile Ser	
435 440 445	
atc gga ctg ttc ttc ctt cat aaa aga ggg atc att tac agg gat ctg	1392
Ile Gly Leu Phe Phe Leu His Lys Arg Gly Ile Ile Tyr Arg Asp Leu	
450 455 460	
aag ctg aac aat gtc atg ctg aac tca gaa ggg cac atc aaa atc gcc	1440
Lys Leu Asn Asn Val Met Leu Asn Ser Glu Gly His Ile Lys Ile Ala	
465 470 475 480	

gac ttc ggg atg tgc aag gaa cac atg atg gat gga gtc acg acc agg	1488
Asp Phe Gly Met Cys Lys Glu His Met Met Asp Gly Val Thr Arg	
485 490 495	
acc ttc tgc gga act ccg gac tac att gcc cca gag ata atc gct tac	1536
Thr Phe Cys Gly Thr Pro Asp Tyr Ile Ala Pro Glu Ile Ile Ala Tyr	
500 505 510	
cag ccg tac ggg aag tct gta gat tgg tgg gcg tac ggt gtg ctg ctg	1584
Gln Pro Tyr Gly Lys Ser Val Asp Trp Trp Ala Tyr Gly Val Leu Leu	
515 520 525	
tac gag atg cta gcc ggg cag cct ccg ttt gat ggt gaa gat gaa gat	1632
Tyr Glu Met Leu Ala Gly Gln Pro Pro Phe Asp Gly Glu Asp Glu Asp	
530 535 540	
gaa ctg ttt cag tct ata atg gag cac aac gtg tcc tac ccc aaa tcc	1680
Glu Leu Phe Gln Ser Ile Met Glu His Asn Val Ser Tyr Pro Lys Ser	
545 550 555 560	
ttg tcc aag gaa gcc gtc tcc atc tgc aaa gga ctt atg acc aaa cag	1728
Leu Ser Lys Glu Ala Val Ser Ile Cys Lys Gly Leu Met Thr Lys Gln	
565 570 575	
cct gcc aag cga ctg ggc tgc ggg ccc gag gga gag agg gat gtc aga	1776
Pro Ala Lys Arg Leu Gly Cys Gly Pro Glu Gly Glu Arg Asp Val Arg	
580 585 590	
gag cat gcc ttc ttc agg agg atc gac tgg gag aaa ctg gag aac agg	1824
Glu His Ala Phe Phe Arg Arg Ile Asp Trp Glu Lys Leu Glu Asn Arg	
595 600 605	
gag atc caa cca cca ttc aag ccc aaa gtg tgt ggc aaa gga gca gaa	1872
Glu Ile Gln Pro Pro Phe Lys Pro Lys Val Cys Gly Lys Gly Ala Glu	
610 615 620	
aac ttt gac aag ttc ttc acg cga gga cag cct gtc tta aca cca cca	1920
Asn Phe Asp Lys Phe Thr Arg Gly Gln Pro Val Leu Thr Pro Pro	
625 630 635 640	
gat cag ctg gtc att gct aac ata gac caa tct gat ttt gaa ggg ttc	1968
Asp Gln Leu Val Ile Ala Asn Ile Asp Gln Ser Asp Phe Glu Gly Phe	
645 650 655	
tcg tat gtc aac ccc cag ttt gtg cac cca atc ttg caa agt gca gta	2016
Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val	
660 665 670	
ggg cgc gcc atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca	2064
Gly Arg Ala Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro	
675 680 685	
att ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt	2112
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val	
690 695 700	
agt gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa	2160
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys	
705 710 715 720	
ttt att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc	2208
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val	
725 730 735	
act act ctc act tat ggt gtt caa tgc ttt tct aga tac cca gat cat	2256
Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His	
740 745 750	
atg aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta	2304
Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val	
755 760 765	
cag gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt	2352
Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg	
770 775 780	
gct gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta	2400
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu	
785 790 795 800	
aaa ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg	2448
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met	
805 810 815	

gaa tac aat tat aac tca cat aat gta tac atc atg gca gac aaa cca	2496
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro	
820 825 830	
aag aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa gat	2544
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp	
835 840 845	
gga agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc	2592
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
850 855 860	
gat ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct	2640
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser	
865 870 875 880	
gcc ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt	2688
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu	
885 890 895	
gag ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac	2736
Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr	
900 905 910	
aaa cct cag gag taa	2751
Lys Pro Gln Glu	
915	

<210> 73

<211> 916

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion construct

<400> 73

Met Ala Asp Val Tyr Pro Ala Asn Asp Ser Thr Ala Ser Gln Asp Val	
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Ala Asn Arg Phe Ala Arg Lys Gly Ala Leu Arg Gln Lys Asn Val His	
20 25 30	
Glu Val Lys Asp His Lys Phe Ile Ala Arg Phe Phe Lys Gln Pro Thr	
35 40 45	
Phe Cys Ser His Cys Thr Asp Phe Ile Trp Gly Phe Gly Lys Gln Gly	
50 55 60	
Phe Gln Cys Gln Val Cys Cys Phe Val Val His Lys Arg Cys His Glu	
65 70 75 80	
Phe Val Thr Phe Ser Cys Pro Gly Ala Asp Lys Gly Pro Asp Thr Asp	
85 90 95	
Asp Pro Arg Ser Lys His Lys Phe Lys Ile His Thr Tyr Gly Ser Pro	
100 105 110	
Thr Phe Cys Asp His Cys Gly Ser Leu Leu Tyr Gly Leu Ile His Gln	
115 120 125	
Gly Met Lys Cys Asp Thr Cys Asp Met Asn Val His Asn Gln Cys Val	
130 135 140	
Ile Asn Asp Pro Ser Leu Cys Gly Met Asp His Thr Glu Lys Arg Gly	
145 150 155 160	
Arg Ile Tyr Leu Lys Ala Glu Val Thr Asp Glu Lys Leu His Val Thr	
165 170 175	
Val Arg Asp Ala Lys Asn Leu Ile Pro Met Asp Pro Asn Gly Leu Ser	
180 185 190	
Asp Pro Tyr Val Lys Leu Lys Leu Ile Pro Asp Pro Lys Asn Glu Ser	



Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys  
 705 710 715 720  
 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val  
 725 730 735  
 Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His  
 740 745 750  
 Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val  
 755 760 765  
 Gln Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg  
 770 775 780  
 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu  
 785 790 795 800  
 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met  
 805 810 815  
 Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro  
 820 825 830  
 Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp  
 835 840 845  
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly  
 850 855 860  
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser  
 865 870 875 880  
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu  
 885 890 895  
 Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr  
 900 905 910  
 Lys Pro Gln Glu  
 915

<210> 74

<211> 2157

<212> DNA

<213> Artificial Sequence

<220>

<223> Smad2-EGFP fusion

<220>

<221> CDS

<222> (1)..(2154)

<400> 74  
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 Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Val Val Lys Arg Leu Leu  
 1 5 10 15  
 gga tgg aag aag tca gct ggt ggg tct gga gga gca ggc gga gga gag 96  
 Gly Trp Lys Lys Ser Ala Gly Gly Ser Gly Gly Ala Gly Gly Gly Glu  
 20 25 30  
 cag aat ggg cag gaa gaa aag tgg tgt gag aaa gca gtg aaa agt ctg 144  
 Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu Lys Ala Val Lys Ser Leu  
 35 40 45  
 gtg aag aag cta aag aaa aca gga cga tta gat gag ctt gag aaa gcc 192

Val	Lys	Lys	Leu	Lys	Lys	Thr	Gly	Arg	Leu	Asp	Glu	Leu	Glu	Lys	Ala		
50						55					60						
atc	acc	act	caa	aac	tgt	aat	act	aaa	tgt	ggt	acc	ata	cca	agc	act	240	
Ile	Thr	Thr	Gln	Asn	Cys	Asn	Thr	Lys	Cys	Val	Thr	Ile	Pro	Ser	Thr		
65					70					75					80		
tgc	tct	gaa	att	tgg	gga	ctg	agt	aca	cca	aat	acg	ata	gat	cag	tgg	288	
Cys	Ser	Glu	Ile	Trp	Gly	Leu	Ser	Thr	Pro	Asn	Thr	Ile	Asp	Gln	Trp		
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gat	aca	aca	ggc	ctt	tac	agc	ttc	tct	gaa	caa	acc	agg	tct	ctt	gat	336	
Asp	Thr	Thr	Gly	Leu	Tyr	Ser	Phe	Ser	Glu	Gln	Thr	Arg	Ser	Leu	Asp		
			100					105					110				
ggt	cgt	ctc	cag	gta	tcc	cat	cga	aaa	gga	ttg	cca	cat	ggt	ata	tat	384	
Gly	Arg	Leu	Gln	Val	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr		
			115				120					125					
tgc	cga	tta	tgg	cgc	tgg	cct	gat	ctt	cac	agt	cat	cat	gaa	ctc	aag	432	
Cys	Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Ser	His	His	Glu	Leu	Lys		
			130			135					140						
gca	att	gaa	aac	tgc	gaa	tat	gct	ttt	aat	ctt	aaa	aag	gat	gaa	gta	480	
Ala	Ile	Glu	Asn	Cys	Glu	Tyr	Ala	Phe	Asn	Leu	Lys	Lys	Asp	Glu	Val		
145				150					155					160			
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Cys	Val	Asn	Pro	Tyr	His	Tyr	Gln	Arg	Val	Glu	Thr	Pro	Val	Leu	Pro		
			165					170					175				
cca	gta	tta	gtg	ccc	cga	cac	acc	gag	atc	cta	aca	gaa	ctt	ccg	cct	576	
Pro	Val	Leu	Val	Pro	Arg	His	Thr	Glu	Ile	Leu	Thr	Glu	Leu	Pro	Pro		
			180					185					190				
ctg	gat	gac	tat	act	cac	tcc	att	cca	gaa	aac	act	aac	ttc	cca	gca	624	
Leu	Asp	Asp	Tyr	Thr	His	Ser	Ile	Pro	Glu	Asn	Thr	Asn	Phe	Pro	Ala		
			195			200					205						
gga	att	gag	cca	cag	agt	aat	tat	att	cca	gaa	acg	cca	cct	cct	gga	672	
Gly	Ile	Glu	Pro	Gln	Ser	Asn	Tyr	Ile	Pro	Glu	Thr	Pro	Pro	Pro	Gly		
			210			215					220						
tat	atc	agt	gaa	gat	gga	gaa	aca	agt	gac	caa	cag	ttg	aat	caa	agt	720	
Tyr	Ile	Ser	Glu	Asp	Gly	Glu	Thr	Ser	Asp	Gln	Gln	Leu	Asn	Gln	Ser		
225				230					235					240			
atg	gac	aca	ggc	tct	cca	gca	gaa	cta	tct	cct	act	act	ctt	tcc	cct	768	
Met	Asp	Thr	Gly	Ser	Pro	Ala	Glu	Leu	Ser	Pro	Thr	Thr	Leu	Ser	Pro		
			245					250					255				
ggt	aat	cat	agc	ttg	gat	tta	cag	cca	ggt	act	tac	tca	gaa	cct	gca	816	
Val	Asn	His	Ser	Leu	Asp	Leu	Gln	Pro	Val	Thr	Tyr	Ser	Glu	Pro	Ala		
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Phe	Trp	Cys	Ser	Ile	Ala	Tyr	Tyr	Glu	Leu	Asn	Gln	Arg	Val	Gly	Glu		
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acc	ttc	cat	gca	tca	cag	ccc	tca	ctc	act	gta	gat	ggc	ttt	aca	gac	912	
Thr	Phe	His	Ala	Ser	Gln	Pro	Ser	Leu	Thr	Val	Asp	Gly	Phe	Thr	Asp		
			290			295					300						
cca	tca	aat	tca	gag	agg	ttc	tgc	tta	ggt	tta	ctc	tcc	aat	ggt	aac	960	
Pro	Ser	Asn	Ser	Glu	Arg	Phe	Cys	Leu	Gly	Leu	Leu	Ser	Asn	Val	Asn		
305				310					315					320			
cga	aat	gcc	acg	gta	gaa	atg	aca	aga	agg	cat	ata	gga	aga	gga	gtg	1008	
Arg	Asn	Ala	Thr	Val	Glu	Met	Thr	Arg	Arg	His	Ile	Gly	Arg	Gly	Val		
			325					330					335				
cgc	tta	tac	tac	ata	ggt	ggg	gaa	ggt	ttt	gct	gag	tgc	cta	agt	gat	1056	
Arg	Leu	Tyr	Tyr	Ile	Gly	Gly	Glu	Val	Phe	Ala	Glu	Cys	Leu	Ser	Asp		
			340			345						350					
agt	gca	atc	ttt	gtg	cag	agc	ccc	aat	tgt	aat	cag	aga	tat	ggc	tgg	1104	
Ser	Ala	Ile	Phe	Val	Gln	Ser	Pro	Asn	Cys	Asn	Gln	Arg	Tyr	Gly	Trp		
			355			360					365						
cac	cct	gca	aca	gtg	tgt	aaa	att	cca	cca	ggc	tgt	aat	ctg	aag	atc	1152	
His	Pro	Ala	Thr	Val	Cys	Lys	Ile	Pro	Pro	Gly	Cys	Asn	Leu	Lys	Ile		
			370			375					380						
ttc	aac	aac	cag	gaa	ttt	gct	gct	ctt	ctg	gct	cag	tct	ggt	aat	cag	1200	



Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln	
385 390 395 400	
ggt ttt gaa gcc gtc tat cag cta act aga atg tgc acc ata aga atg	1248
Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met	
405 410 415	
agt ttt gtg aaa ggg tgg gga gca gaa tac cga agg cag acg gta aca	1296
Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr	
420 425 430	
agt act cct tgc tgg att gaa ctt cat ctg aat gga cct cta cag tgg	1344
Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp	
435 440 445	
ttg gac aaa gta tta act cag atg gga tcc cct tca gtg cgt tgc tca	1392
Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser	
450 455 460	
agc atg tca tgg gta ccg cgg gcc cgg gat cca ccg gtc gcc acc atg	1440
Ser Met Ser Trp Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met	
465 470 475 480	
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
485 490 495	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	1536
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
515 520 525	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	1632
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
530 535 540	
acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag	1680
Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
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His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
565 570 575	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	1776
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
580 585 590	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	1824
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
595 600 605	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	1872
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
610 615 620	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	1920
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
625 630 635 640	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	1968
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
645 650 655	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc	2016
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	
660 665 670	
gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc	2064
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser	
675 680 685	
aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg	2112
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val	
690 695 700	
acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa	2157
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<212> PRT

<213> Artificial Sequence

<220>

<223> Smad2-EGFP fusion

<400> 75

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Gly	Trp	Lys	Lys	Ser	Ala	Gly	Gly	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Glu
			20					25					30		
Gln	Asn	Gly	Gln	Glu	Glu	Lys	Trp	Cys	Glu	Lys	Ala	Val	Lys	Ser	Leu
		35					40					45			
Val	Lys	Lys	Leu	Lys	Lys	Thr	Gly	Arg	Leu	Asp	Glu	Leu	Glu	Lys	Ala
	50					55					60				
Ile	Thr	Thr	Gln	Asn	Cys	Asn	Thr	Lys	Cys	Val	Thr	Ile	Pro	Ser	Thr
65				70						75					80
Cys	Ser	Glu	Ile	Trp	Gly	Leu	Ser	Thr	Pro	Asn	Thr	Ile	Asp	Gln	Trp
			85						90					95	
Asp	Thr	Thr	Gly	Leu	Tyr	Ser	Phe	Ser	Glu	Gln	Thr	Arg	Ser	Leu	Asp
			100					105					110		
Gly	Arg	Leu	Gln	Val	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr
	115					120						125			
Cys	Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Ser	His	His	Glu	Leu	Lys
	130					135					140				
Ala	Ile	Glu	Asn	Cys	Glu	Tyr	Ala	Phe	Asn	Leu	Lys	Lys	Asp	Glu	Val
145					150					155					160
Cys	Val	Asn	Pro	Tyr	His	Tyr	Gln	Arg	Val	Glu	Thr	Pro	Val	Leu	Pro
			165					170						175	
Pro	Val	Leu	Val	Pro	Arg	His	Thr	Glu	Ile	Leu	Thr	Glu	Leu	Pro	Pro
		180						185					190		
Leu	Asp	Asp	Tyr	Thr	His	Ser	Ile	Pro	Glu	Asn	Thr	Asn	Phe	Pro	Ala
	195					200						205			
Gly	Ile	Glu	Pro	Gln	Ser	Asn	Tyr	Ile	Pro	Glu	Thr	Pro	Pro	Pro	Gly
	210					215						220			
Tyr	Ile	Ser	Glu	Asp	Gly	Glu	Thr	Ser	Asp	Gln	Gln	Leu	Asn	Gln	Ser
225				230						235					240
Met	Asp	Thr	Gly	Ser	Pro	Ala	Glu	Leu	Ser	Pro	Thr	Thr	Leu	Ser	Pro
			245					250					255		
Val	Asn	His	Ser	Leu	Asp	Leu	Gln	Pro	Val	Thr	Tyr	Ser	Glu	Pro	Ala
		260						265					270		
Phe	Trp	Cys	Ser	Ile	Ala	Tyr	Tyr	Glu	Leu	Asn	Gln	Arg	Val	Gly	Glu
	275					280						285			
Thr	Phe	His	Ala	Ser	Gln	Pro	Ser	Leu	Thr	Val	Asp	Gly	Phe	Thr	Asp
	290				295						300				
Pro	Ser	Asn	Ser	Glu	Arg	Phe	Cys	Leu	Gly	Leu	Ser	Asn	Val	Asn	
305				310						315				320	
Arg	Asn	Ala	Thr	Val	Glu	Met	Thr	Arg	Arg	His	Ile	Gly	Arg	Gly	Val
			325						330					335	
Arg	Leu	Tyr	Tyr	Ile	Gly	Gly	Glu	Val	Phe	Ala	Glu	Cys	Leu	Ser	Asp
		340					345						350		
Ser	Ala	Ile	Phe	Val	Gln	Ser	Pro	Asn	Cys	Asn	Gln	Arg	Tyr	Gly	Trp
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His	Pro	Ala	Thr	Val	Cys	Lys	Ile	Pro	Pro	Gly	Cys	Asn	Leu	Lys	Ile



<222> (1)..(2394)

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ctg agc att gtg cat agt ttg atg tgc cat aga caa ggt gga gag agt      96
Leu Ser Ile Val His Ser Leu Met Cys His Arg Gln Gly Gly Glu Ser
20      25      30
gaa aca ttt gca aaa aga gca att gaa agt ttg gta aag aag ctg aag      144
Glu Thr Phe Ala Lys Arg Ala Ile Glu Ser Leu Val Lys Lys Leu Lys
35      40      45
gag aaa aaa gat gaa ttg gat tct tta ata aca gct ata act aca aat      192
Glu Lys Lys Asp Glu Leu Asp Ser Leu Ile Thr Ala Ile Thr Thr Asn
50      55      60
gga gct cat cct agt aaa tgt gtt acc ata cag aga aca ttg gat ggg      240
Gly Ala His Pro Ser Lys Cys Val Thr Ile Gln Arg Thr Leu Asp Gly
65      70      75      80
agg ctt cag gtg gct ggt cgg aaa gga ttt cct cat gtg atc tat gcc      288
Arg Leu Gln Val Ala Gly Arg Lys Gly Phe Pro His Val Ile Tyr Ala
85      90      95
cgt ctc tgg agg tgg cct gat ctt cac aaa aat gaa cta aaa cat gtt      336
Arg Leu Trp Arg Trp Pro Asp Leu His Lys Asn Glu Leu Lys His Val
100      105      110
aaa tat tgt cag tat gcg ttt gac tta aaa tgt gat agt gtc tgt gtg      384
Lys Tyr Cys Gln Tyr Ala Phe Asp Leu Lys Cys Asp Ser Val Cys Val
115      120      125
aat cca tat cac tac gaa cga gtt gta tca cct gga att gat ctc tca      432
Asn Pro Tyr His Tyr Glu Arg Val Val Ser Pro Gly Ile Asp Leu Ser
130      135      140
gga tta aca ctg cag agt aat gct cca tca agt atg atg gtg aag gat      480
Gly Leu Thr Leu Gln Ser Asn Ala Pro Ser Ser Met Met Val Lys Asp
145      150      155      160
gaa tat gtg cat gac ttt gag gga cag cca tcg ttg tcc act gaa gga      528
Glu Tyr Val His Asp Phe Glu Gly Gln Pro Ser Leu Ser Thr Glu Gly
165      170      175
cat tca att caa acc atc cag cat cca cca agt aat cgt gca tcg aca      576
His Ser Ile Gln Thr Ile Gln His Pro Pro Ser Asn Arg Ala Ser Thr
180      185      190
gag aca tac agc acc cca gct ctg tta gcc cca tct gag tct aat gct      624
Glu Thr Tyr Ser Thr Pro Ala Leu Leu Ala Pro Ser Glu Ser Asn Ala
195      200      205
acc agc act gcc aac ttt ccc aac att cct gtg gct tcc aca agt cag      672
Thr Ser Thr Ala Asn Phe Pro Asn Ile Pro Val Ala Ser Thr Ser Gln
210      215      220
cct gcc agt ata ctg ggg ggc agc cat agt gaa gga ctg ttg cag ata      720
Pro Ala Ser Ile Leu Gly Gly Ser His Ser Glu Gly Leu Leu Gln Ile
225      230      235      240
gca tca ggg cct cag cca gga cag cag cag aat gga ttt act ggt cag      768
Ala Ser Gly Pro Gln Pro Gly Gln Gln Asn Gly Phe Thr Gly Gln
245      250      255
cca gct act tac cat cat aac agc act acc acc tgg act gga agt agg      816
Pro Ala Thr Tyr His His Asn Ser Thr Thr Thr Trp Thr Gly Ser Arg
260      265      270
act gca cca tac aca cct aat ttg cct cac cac caa aac ggc cat ctt      864
Thr Ala Pro Tyr Thr Pro Asn Leu Pro His His Gln Asn Gly His Leu
275      280      285
cag cac cac ccg cct atg ccg ccc cat ccc gga cat tac tgg cct gtt      912
Gln His His Pro Pro Met Pro Pro His Pro Gly His Tyr Trp Pro Val
290      295      300
cac aat gag ctt gca ttc cag cct ccc att tcc aat cat cct gct cct      960

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His Asn Glu Leu Ala Phe Gln Pro Pro Ile Ser Asn His Pro Ala Pro	
305 310 315 320	
gag tat tgg tgt tcc att gct tac ttt gaa atg gat gtt cag gta gga	1008
Glu Tyr Trp Cys Ser Ile Ala Tyr Phe Glu Met Asp Val Gln Val Gly	
325 330 335	
gag aca ttt aag gtt cct tca agc tgc cct att gtt act gtt gat gga	1056
Glu Thr Phe Lys Val Pro Ser Ser Cys Pro Ile Val Thr Val Asp Gly	
340 345 350	
tac gtg gac cct tct gga gga gat cgc ttt tgt ttg ggt caa ctc tcc	1104
Tyr Val Asp Pro Ser Gly Gly Asp Arg Phe Cys Leu Gly Gln Leu Ser	
355 360 365	
aat gtc cac agg aca gaa gcc att gag aga gca agg ttg cac ata ggc	1152
Asn Val His Arg Thr Glu Ala Ile Glu Arg Ala Arg Leu His Ile Gly	
370 375 380	
aaa ggt gtg cag ttg gaa tgt aaa ggt gaa ggt gat gtt ttg gtc agg	1200
Lys Gly Val Gln Leu Glu Cys Lys Gly Glu Gly Asp Val Trp Val Arg	
385 390 395 400	
tgc ctt agt gac cac gcg gtc ttt gta cag agt tac tac tta gac aga	1248
Cys Leu Ser Asp His Ala Val Phe Val Gln Ser Tyr Tyr Leu Asp Arg	
405 410 415	
gaa gct ggg cgt gca cct gga gat gct gtt cat aag atc tac cca agt	1296
Glu Ala Gly Arg Ala Pro Gly Asp Ala Val His Lys Ile Tyr Pro Ser	
420 425 430	
gca tat ata aag gtc ttt gat ttg cgt cag tgt cat cga cag atg cag	1344
Ala Tyr Ile Lys Val Phe Asp Leu Arg Gln Cys His Arg Gln Met Gln	
435 440 445	
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Gln Gln Ala Ala Thr Ala Gln Ala Ala Ala Ala Gln Ala Ala Ala	
450 455 460	
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Val Ala Gly Asn Ile Pro Gly Pro Gly Ser Val Gly Gly Ile Ala Pro	
465 470 475 480	
gct atc agt ctg tca gct gct gct gga att ggt gtt gat gac ctt cgt	1488
Ala Ile Ser Leu Ser Ala Ala Ala Gly Ile Gly Val Asp Asp Leu Arg	
485 490 495	
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Arg Leu Cys Ile Leu Arg Met Ser Phe Val Lys Gly Trp Gly Pro Asp	
500 505 510	
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Tyr Pro Arg Gln Ser Ile Lys Glu Thr Pro Cys Trp Ile Glu Ile His	
515 520 525	
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Leu His Arg Ala Leu Gln Leu Leu Asp Glu Val Leu His Thr Met Pro	
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Ile Ala Asp Pro Gln Pro Leu Asp Trp Asp Pro Pro Val Ala Thr Met	
545 550 555 560	
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Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
565 570 575	
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
580 585 590	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	1824
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
595 600 605	
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Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
610 615 620	
acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag	1920
Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
625 630 635 640	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	1968

His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
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Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
				660				665					670				
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	2064	
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
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gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	2112	
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
				690				695					700				
tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	2160	
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly		
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atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	2208	
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val		
				725											735		
cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	2256	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro		
					740										750		
gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	agc	2304	
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser		
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aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	2352	
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val		
						775									780		
acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	taa		2397	
Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys				
					790										795		

<210> 77

<211> 798

<212> PRT

<213> Artificial Sequence

<220>

<223> Smad4-EGFP fusion

<400> 77

Met	Asp	Asn	Met	Ser	Ile	Thr	Asn	Thr	Pro	Thr	Ser	Asn	Asp	Ala	Cys		
1				5					10					15			
Leu	Ser	Ile	Val	His	Ser	Leu	Met	Cys	His	Arg	Gln	Gly	Gly	Glu	Ser		
				20				25						30			
Glu	Thr	Phe	Ala	Lys	Arg	Ala	Ile	Glu	Ser	Leu	Val	Lys	Lys	Leu	Lys		
				35				40						45			
Glu	Lys	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Ile	Thr	Ala	Ile	Thr	Thr	Asn		
				50				55						60			
Gly	Ala	His	Pro	Ser	Lys	Cys	Val	Thr	Ile	Gln	Arg	Thr	Leu	Asp	Gly		
					70					75				80			
Arg	Leu	Gln	Val	Ala	Gly	Arg	Lys	Gly	Phe	Pro	His	Val	Ile	Tyr	Ala		
				85					90					95			
Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Lys	Asn	Glu	Leu	Lys	His	Val		
				100				105						110			
Lys	Tyr	Cys	Gln	Tyr	Ala	Phe	Asp	Leu	Lys	Cys	Asp	Ser	Val	Cys	Val		
				115				120						125			
Asn	Pro	Tyr	His	Tyr	Glu	Arg	Val	Val	Ser	Pro	Gly	Ile	Asp	Leu	Ser		

130					135					140							
Gly	Leu	Thr	Leu	Gln	Ser	Asn	Ala	Pro	Ser	Ser	Met	Met	Val	Lys	Asp		
145					150					155					160		
Glu	Tyr	Val	His	Asp	Phe	Glu	Gly	Gln	Pro	Ser	Leu	Ser	Thr	Glu	Gly		
				165					170					175			
His	Ser	Ile	Gln	Thr	Ile	Gln	His	Pro	Pro	Ser	Asn	Arg	Ala	Ser	Thr		
			180					185					190				
Glu	Thr	Tyr	Ser	Thr	Pro	Ala	Leu	Leu	Ala	Pro	Ser	Glu	Ser	Asn	Ala		
		195					200					205					
Thr	Ser	Thr	Ala	Asn	Phe	Pro	Asn	Ile	Pro	Val	Ala	Ser	Thr	Ser	Gln		
	210					215				220							
Pro	Ala	Ser	Ile	Leu	Gly	Gly	Ser	His	Ser	Glu	Gly	Leu	Leu	Gln	Ile		
225					230					235				240			
Ala	Ser	Gly	Pro	Gln	Pro	Gly	Gln	Gln	Gln	Asn	Gly	Phe	Thr	Gly	Gln		
				245					250					255			
Pro	Ala	Thr	Tyr	His	His	Asn	Ser	Thr	Thr	Thr	Trp	Thr	Gly	Ser	Arg		
			260					265					270				
Thr	Ala	Pro	Tyr	Thr	Pro	Asn	Leu	Pro	His	His	Gln	Asn	Gly	His	Leu		
	275						280					285					
Gln	His	Pro	Pro	Met	Pro	Pro	His	Pro	Gly	His	Tyr	Trp	Pro	Val			
290					295					300							
His	Asn	Glu	Leu	Ala	Phe	Gln	Pro	Pro	Ile	Ser	Asn	His	Pro	Ala	Pro		
305					310					315				320			
Glu	Tyr	Trp	Cys	Ser	Ile	Ala	Tyr	Phe	Glu	Met	Asp	Val	Gln	Val	Gly		
				325					330					335			
Glu	Thr	Phe	Lys	Val	Pro	Ser	Ser	Cys	Pro	Ile	Val	Thr	Val	Asp	Gly		
			340					345				350					
Tyr	Val	Asp	Pro	Ser	Gly	Gly	Asp	Arg	Phe	Cys	Leu	Gly	Gln	Leu	Ser		
	355						360				365						
Asn	Val	His	Arg	Thr	Glu	Ala	Ile	Glu	Arg	Ala	Arg	Leu	His	Ile	Gly		
	370				375						380						
Lys	Gly	Val	Gln	Leu	Glu	Cys	Lys	Gly	Glu	Gly	Asp	Val	Trp	Val	Arg		
385					390					395				400			
Cys	Leu	Ser	Asp	His	Ala	Val	Phe	Val	Gln	Ser	Tyr	Tyr	Leu	Asp	Arg		
				405					410					415			
Glu	Ala	Gly	Arg	Ala	Pro	Gly	Asp	Ala	Val	His	Lys	Ile	Tyr	Pro	Ser		
			420					425				430					
Ala	Tyr	Ile	Lys	Val	Phe	Asp	Leu	Arg	Gln	Cys	His	Arg	Gln	Met	Gln		
	435						440					445					
Gln	Gln	Ala	Ala	Thr	Ala	Gln	Ala	Ala	Ala	Ala	Ala	Gln	Ala	Ala	Ala		
	450					455					460						
Val	Ala	Gly	Asn	Ile	Pro	Gly	Pro	Gly	Ser	Val	Gly	Gly	Ile	Ala	Pro		
465					470					475				480			
Ala	Ile	Ser	Leu	Ser	Ala	Ala	Ala	Gly	Ile	Gly	Val	Asp	Asp	Leu	Arg		
				485					490					495			
Arg	Leu	Cys	Ile	Leu	Arg	Met	Ser	Phe	Val	Lys	Gly	Trp	Gly	Pro	Asp		
				500				505				510					
Tyr	Pro	Arg	Gln	Ser	Ile	Lys	Glu	Thr	Pro	Cys	Trp	Ile	Glu	Ile	His		
	515						520					525					
Leu	His	Arg	Ala	Leu	Gln	Leu	Leu	Asp	Glu	Val	Leu	His	Thr	Met	Pro		
	530					535					540						
Ile	Ala	Asp	Pro	Gln	Pro	Leu	Asp	Trp	Asp	Pro	Pro	Val	Ala	Thr	Met		
545					550					555				560			
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
				565					570					575			
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
			580					585					590				
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
		595					600					605					
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu		
	610					615						620					
Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln		
625					630					635					640		

His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				645					650					655	
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
			660					665						670	
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
		675					680							685	
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
	690					695					700				
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
705					710					715					720
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
			725						730					735	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
			740					745						750	
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
		755					760							765	
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	770					775					780				
Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
785					790					795					

<210> 78

<211> 3138

<212> DNA

<213> Artificial Sequence

<220>

<223> Stat5-EGFP fusion construct

<220>

<221> CDS

<222> (1)..(3135)

<400>	78	
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1 5 10 15		
cag atg cag gtg ctg tac ggc cag cac ttc ccc atc gag gtc cgg cac		96
Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro Ile Glu Val Arg His		
20 25 30		
tac ttg gcc cag tgg att gag agc cag cca tgg gat gcc att gac ttg		144
Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp Asp Ala Ile Asp Leu		
35 40 45		
gac aat ccc cag gac aga gcc caa gcc acc cag ctc ctg gag ggc ctg		192
Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln Leu Leu Glu Gly Leu		
50 55 60		
gtg cag gag ctg cag aag aag gcg gag cac cag gtg ggg gaa gat ggg		240
Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln Val Gly Glu Asp Gly		
65 70 75 80		
ttt tta ctg aag atc aag ctg ggg cac tac gcc acg cag ctc cag aaa		288
Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala Thr Gln Leu Gln Lys		
85 90 95		



aca tat gac cgc tgc ccc ctg gag ctg gtc cgc tgc atc cgg cac att	336
Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg Cys Ile Arg His Ile	
100 105 110	
ctg tac aat gaa cag agg ctg gtc cga gaa gcc aac aat tgc agc tct	384
Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala Asn Asn Cys Ser Ser	
115 120 125	
ccg gct ggg atc ctg gtt gac gcc atg tcc cag aag cac ctt cag atc	432
Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln Lys His Leu Gln Ile	
130 135 140	
aac cag aca ttt gag gag ctg cga ctg gtc acg cag gac aca gag aat	480
Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr Gln Asp Thr Glu Asn	
145 150 155 160	
gag ctg aag aaa ctg cag cag act cag gag tac ttc atc atc cag tac	528
Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr Phe Ile Ile Gln Tyr	
165 170 175	
cag gag agc ctg agg atc caa gct cag ttt gcc cag ctg gcc cag ctg	576
Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala Gln Leu Ala Gln Leu	
180 185 190	
agc ccc cag gag cgt ctg agc cgg gag acg gcc ctc cag cag aag cag	624
Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala Leu Gln Lys Gln	
195 200 205	
gtg tct ctg gag gcc tgg ttg cag cgt gag gca cag aca ctg cag cag	672
Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala Gln Thr Leu Gln Gln	
210 215 220	
tac cgc gtg gag ctg gcc gag aag cac cag aag acc ctg cag ctg ctg	720
Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys Thr Leu Gln Leu Leu	
225 230 235 240	
cgg aag cag cag acc atc atc ctg gat gac gag ctg atc cag tgg aag	768
Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu Leu Ile Gln Trp Lys	
245 250 255	
cgg cgg cag cag ctg gcc ggg aac ggc ggg ccc ccc gag ggc agc ctg	816
Arg Arg Gln Gln Leu Ala Gly Asn Gly Gly Pro Pro Glu Gly Ser Leu	
260 265 270	
gac gtg cta cag tcc tgg tgt gag aag ttg gcc gag atc atc tgg cag	864
Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala Glu Ile Ile Trp Gln	
275 280 285	
aac cgg cag cag atc cgc agg gct gag cac ctc tgc cag cag ctg ccc	912
Asn Arg Gln Gln Ile Arg Arg Ala Glu His Leu Cys Gln Gln Leu Pro	
290 295 300	
atc ccc ggc cca gtg gag gag atg ctg gcc gag gtc aac gcc acc atc	960
Ile Pro Gly Pro Val Glu Glu Met Leu Ala Glu Val Asn Ala Thr Ile	
305 310 315 320	
acg gac att atc tca gcc ctg gtg acc agc aca ttc atc att gag aag	1008
Thr Asp Ile Ile Ser Ala Leu Val Thr Ser Thr Phe Ile Ile Glu Lys	
325 330 335	
cag cct cct cag gtc ctg aag acc cag acc aag ttt gca gcc acc gta	1056
Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys Phe Ala Ala Thr Val	
340 345 350	
cgc ctg ctg gtg ggc ggg aag ctg aac gtg cac atg aat ccc ccc cag	1104
Arg Leu Leu Val Gly Gly Lys Leu Asn Val His Met Asn Pro Pro Gln	
355 360 365	
gtg aag gcc acc atc atc agt gag cag cag gcc aag tct ctg ctt aaa	1152
Val Lys Ala Thr Ile Ile Ser Glu Gln Gln Ala Lys Ser Leu Leu Lys	
370 375 380	
aat gag aac acc cgc aac gag tgc agt ggt gag atc ctg aac aac tgc	1200
Asn Glu Asn Thr Arg Asn Glu Cys Ser Gly Glu Ile Leu Asn Asn Cys	
385 390 395 400	
tgc gtg atg gag tac cac caa gcc acg ggc acc ctc agt gcc cac ttc	1248
Cys Val Met Glu Tyr His Gln Ala Thr Gly Thr Leu Ser Ala His Phe	
405 410 415	
agg aac atg tca ctg aag agg atc aag cgt gct gac cgg cgg ggt gca	1296
Arg Asn Met Ser Leu Lys Arg Ile Lys Arg Ala Asp Arg Arg Gly Ala	
420 425 430	

gag tcc gtg aca gag gag aag ttc aca gtc ctg ttt gag tct cag ttc	1344
Glu Ser Val Thr Glu Glu Lys Phe Thr Val Leu Phe Glu Ser Gln Phe	
435 440 445	
agt gtt ggc agc aat gag ctt gtg ttc cag gtg aag act ctg tcc cta	1392
Ser Val Gly Ser Asn Glu Leu Val Phe Gln Val Lys Thr Leu Ser Leu	
450 455 460	
cct gtg gtt gtc atc gtc cac ggc agc cag gac cac aat gcc acg gct	1440
Pro Val Val Val Ile Val His Gly Ser Gln Asp His Asn Ala Thr Ala	
465 470 475 480	
act gtg ctg tgg gac aat gcc ttt gct gag ccg ggc agg gtg cca ttt	1488
Thr Val Leu Trp Asp Asn Ala Phe Ala Glu Pro Gly Arg Val Pro Phe	
485 490 495	
gcc gtg cct gac aaa gtg ctg tgg ccg cag ctg tgt gag gcg ctc aac	1536
Ala Val Pro Asp Lys Val Leu Trp Pro Gln Leu Cys Glu Ala Leu Asn	
500 505 510	
atg aaa ttc aag gcc gaa gtg cag agc aac cgg ggc ctg acc aag gag	1584
Met Lys Phe Lys Ala Glu Val Gln Ser Asn Arg Gly Leu Thr Lys Glu	
515 520 525	
aac ctc gtg ttc ctg gcg cag aaa ctg ttc aac aac agc agc cac	1632
Asn Leu Val Phe Leu Ala Gln Lys Leu Phe Asn Asn Ser Ser Ser His	
530 535 540	
ctg gag gac tac agt ggc ctg tcc gtg tcc tgg tcc cag ttc aac agg	1680
Leu Glu Asp Tyr Ser Gly Leu Ser Val Ser Trp Ser Gln Phe Asn Arg	
545 550 555 560	
gag aac ttg ccg ggc tgg aac tac acc ttc tgg cag tgg ttt gac ggg	1728
Glu Asn Leu Pro Gly Trp Asn Tyr Thr Phe Trp Gln Trp Phe Asp Gly	
565 570 575	
gtg atg gag gtg ttg aag aag cac cac aag ccc cac tgg aat gat ggg	1776
Val Met Glu Val Leu Lys Lys His His Lys Pro His Trp Asn Asp Gly	
580 585 590	
gcc atc cta ggt ttt gtg aat aag caa cag gcc cac gac ctg ctc atc	1824
Ala Ile Leu Gly Phe Val Asn Lys Gln Gln Ala His Asp Leu Leu Ile	
595 600 605	
aac aag ccc gac ggg acc ttc ttg ttg cgc ttt agt gac tca gaa atc	1872
Asn Lys Pro Asp Gly Thr Phe Leu Leu Arg Phe Ser Asp Ser Glu Ile	
610 615 620	
ggg ggc atc acc atc gcc tgg aag ttt gac tcc ccg gaa cgc aac ctg	1920
Gly Gly Ile Thr Ile Ala Trp Lys Phe Asp Ser Pro Glu Arg Asn Leu	
625 630 635 640	
tgg aac ctg aaa cca ttc acc acg cgg gat ttc tcc atc agg tcc ctg	1968
Trp Asn Leu Lys Pro Phe Thr Thr Arg Asp Phe Ser Ile Arg Ser Leu	
645 650 655	
gct gac cgg ctg ggg gac ctg agc tat ctc atc tat gtg ttt cct gac	2016
Ala Asp Arg Leu Gly Asp Leu Ser Tyr Leu Ile Tyr Val Phe Pro Asp	
660 665 670	
cgc ccc aag gat gag gtc ttc tcc aag tac tac act cct gtg ctg gct	2064
Arg Pro Lys Asp Glu Val Phe Ser Lys Tyr Tyr Thr Pro Val Leu Ala	
675 680 685	
aaa gct gtt gat gga tat gtg aaa cca cag atc aag caa gtg gtc cct	2112
Lys Ala Val Asp Gly Tyr Val Lys Pro Gln Ile Lys Gln Val Val Pro	
690 695 700	
gag ttt gtg aat gca tct gca gat gct ggg ggc agc agc gcc acg tac	2160
Glu Phe Val Asn Ala Ser Ala Asp Ala Gly Gly Ser Ser Ala Thr Tyr	
705 710 715 720	
atg gac cag gcc ccc tcc cca gct gtg tgc ccc cag gct ccc tat aac	2208
Met Asp Gln Ala Pro Ser Pro Ala Val Cys Pro Gln Ala Pro Tyr Asn	
725 730 735	
atg tac cca cag aac cct gac cat gta ctc gat cag gat gga gaa ttc	2256
Met Tyr Pro Gln Asn Pro Asp His Val Leu Asp Gln Asp Gly Glu Phe	
740 745 750	
gac ctg gat gag acc atg gat gtg gcc agg cac gtg gag gaa ctc tta	2304
Asp Leu Asp Glu Thr Met Asp Val Ala Arg His Val Glu Glu Leu Leu	
755 760 765	

cgc cga cca atg gac agt ctt gac tcc cgc ctc tcg ccc cct gcc ggt	2352
Arg Arg Pro Met Asp Ser Leu Asp Ser Arg Leu Ser Pro Pro Ala Gly	
770 775 780	
ctt ttc acc tct gcc aga ggc tcc ctc tca tgg gta ccg cgg gcc cgg	2400
Leu Phe Thr Ser Ala Arg Gly Ser Leu Ser Trp Val Pro Arg Ala Arg	
785 790 795 800	
gat cca ccg gtc gcc acc atg gtg agc aag ggc gag gag ctg ttc acc	2448
Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr	
805 810 815	
ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac	2496
Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His	
820 825 830	
aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag	2544
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys	
835 840 845	
ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg	2592
Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp	
850 855 860	
ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag tgc ttc agc cgc	2640
Pro Thr Leu Val Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg	
865 870 875 880	
tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg ccc	2688
Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro	
885 890 895	
gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac	2736
Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn	
900 905 910	
tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac	2784
Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn	
915 920 925	
cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg	2832
Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu	
930 935 940	
ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat atc atg	2880
Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met	
945 950 955 960	
gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac	2928
Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His	
965 970 975	
aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac	2976
Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn	
980 985 990	
acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg	3024
Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu	
995 1000 1005	
agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat	3069
Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp	
1010 1015 1020	
cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc	3114
His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu	
1025 1030 1035	
ggc atg gac gag ctg tac aag taa	3138
Gly Met Asp Glu Leu Tyr Lys	
1040 1045	

<210> 79

<211> 1045

<212> PRT

<213> Artificial Sequence

<220>

<223> Stat5-EGFP fusion construct

<400> 79

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Gln	Met	Gln	Val	Leu	Tyr	Gly	Gln	His	Phe	Pro	Ile	Glu	Val	Arg	His
			20					25					30		
Tyr	Leu	Ala	Gln	Trp	Ile	Glu	Ser	Gln	Pro	Trp	Asp	Ala	Ile	Asp	Leu
		35					40					45			
Asp	Asn	Pro	Gln	Asp	Arg	Ala	Gln	Ala	Thr	Gln	Leu	Leu	Glu	Gly	Leu
	50					55					60				
Val	Gln	Glu	Leu	Gln	Lys	Ala	Glu	His	Gln	Val	Gly	Glu	Asp	Gly	
65					70				75					80	
Phe	Leu	Leu	Lys	Ile	Lys	Leu	Gly	His	Tyr	Ala	Thr	Gln	Leu	Gln	Lys
				85					90					95	
Thr	Tyr	Asp	Arg	Cys	Pro	Leu	Glu	Leu	Val	Arg	Cys	Ile	Arg	His	Ile
			100					105					110		
Leu	Tyr	Asn	Glu	Gln	Arg	Leu	Val	Arg	Glu	Ala	Asn	Asn	Cys	Ser	Ser
		115					120					125			
Pro	Ala	Gly	Ile	Leu	Val	Asp	Ala	Met	Ser	Gln	Lys	His	Leu	Gln	Ile
		130				135						140			
Asn	Gln	Thr	Phe	Glu	Glu	Leu	Arg	Leu	Val	Thr	Gln	Asp	Thr	Glu	Asn
145					150					155					160
Glu	Leu	Lys	Lys	Leu	Gln	Gln	Thr	Gln	Glu	Tyr	Phe	Ile	Ile	Gln	Tyr
			165						170					175	
Gln	Glu	Ser	Leu	Arg	Ile	Gln	Ala	Gln	Phe	Ala	Gln	Leu	Ala	Gln	Leu
			180					185					190		
Ser	Pro	Gln	Glu	Arg	Leu	Ser	Arg	Glu	Thr	Ala	Leu	Gln	Gln	Lys	Gln
		195					200					205			
Val	Ser	Leu	Glu	Ala	Trp	Leu	Gln	Arg	Glu	Ala	Gln	Thr	Leu	Gln	Gln
		210					215					220			
Tyr	Arg	Val	Glu	Leu	Ala	Glu	Lys	His	Gln	Lys	Thr	Leu	Gln	Leu	Leu
225					230					235					240
Arg	Lys	Gln	Gln	Thr	Ile	Ile	Leu	Asp	Asp	Glu	Leu	Ile	Gln	Trp	Lys
			245						250					255	
Arg	Arg	Gln	Gln	Leu	Ala	Gly	Asn	Gly	Gly	Pro	Pro	Glu	Gly	Ser	Leu
			260				265						270		
Asp	Val	Leu	Gln	Ser	Trp	Cys	Glu	Lys	Leu	Ala	Glu	Ile	Ile	Trp	Gln
		275				280						285			
Asn	Arg	Gln	Gln	Ile	Arg	Arg	Ala	Glu	His	Leu	Cys	Gln	Gln	Leu	Pro
		290				295					300				
Ile	Pro	Gly	Pro	Val	Glu	Met	Leu	Ala	Glu	Val	Asn	Ala	Thr	Ile	
305					310					315				320	
Thr	Asp	Ile	Ile	Ser	Ala	Leu	Val	Thr	Ser	Thr	Phe	Ile	Ile	Glu	Lys
			325						330					335	
Gln	Pro	Pro	Gln	Val	Leu	Lys	Thr	Gln	Thr	Lys	Phe	Ala	Ala	Thr	Val
			340					345					350		
Arg	Leu	Leu	Val	Gly	Gly	Lys	Leu	Asn	Val	His	Met	Asn	Pro	Pro	Gln
		355					360					365			
Val	Lys	Ala	Thr	Ile	Ile	Ser	Glu	Gln	Gln	Ala	Lys	Ser	Leu	Leu	Lys
		370				375					380				
Asn	Glu	Asn	Thr	Arg	Asn	Glu	Cys	Ser	Gly	Glu	Ile	Leu	Asn	Asn	Cys
385					390					395					400
Cys	Val	Met	Glu	Tyr	His	Gln	Ala	Thr	Gly	Thr	Leu	Ser	Ala	His	Phe
			405						410					415	
Arg	Asn	Met	Ser	Leu	Lys	Arg	Ile	Lys	Arg	Ala	Asp	Arg	Arg	Gly	Ala
			420					425						430	

Glu	Ser	Val	Thr	Glu	Glu	Lys	Phe	Thr	Val	Leu	Phe	Glu	Ser	Gln	Phe
		435					440					445			
Ser	Val	Gly	Ser	Asn	Glu	Leu	Val	Phe	Gln	Val	Lys	Thr	Leu	Ser	Leu
	450					455					460				
Pro	Val	Val	Val	Ile	Val	His	Gly	Ser	Gln	Asp	His	Asn	Ala	Thr	Ala
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Thr	Val	Leu	Trp	Asp	Asn	Ala	Phe	Ala	Glu	Pro	Gly	Arg	Val	Pro	Phe
				485					490					495	
Ala	Val	Pro	Asp	Lys	Val	Leu	Trp	Pro	Gln	Leu	Cys	Glu	Ala	Leu	Asn
			500					505					510		
Met	Lys	Phe	Lys	Ala	Glu	Val	Gln	Ser	Asn	Arg	Gly	Leu	Thr	Lys	Glu
		515					520					525			
Asn	Leu	Val	Phe	Leu	Ala	Gln	Lys	Leu	Phe	Asn	Asn	Ser	Ser	Ser	His
	530					535					540				
Leu	Glu	Asp	Tyr	Ser	Gly	Leu	Ser	Val	Ser	Trp	Ser	Gln	Phe	Asn	Arg
545					550					555					560
Glu	Asn	Leu	Pro	Gly	Trp	Asn	Tyr	Thr	Phe	Trp	Gln	Trp	Phe	Asp	Gly
				565					570					575	
Val	Met	Glu	Val	Leu	Lys	Lys	His	His	Lys	Pro	His	Trp	Asn	Asp	Gly
			580					585					590		
Ala	Ile	Leu	Gly	Phe	Val	Asn	Lys	Gln	Gln	Ala	His	Asp	Leu	Leu	Ile
		595					600					605			
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	610					615					620				
Gly	Gly	Ile	Thr	Ile	Ala	Trp	Lys	Phe	Asp	Ser	Pro	Glu	Arg	Asn	Leu
625					630					635					640
Trp	Asn	Leu	Lys	Pro	Phe	Thr	Thr	Arg	Asp	Phe	Ser	Ile	Arg	Ser	Leu
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Ala	Asp	Arg	Leu	Gly	Asp	Leu	Ser	Tyr	Leu	Ile	Tyr	Val	Phe	Pro	Asp
			660					665					670		
Arg	Pro	Lys	Asp	Glu	Val	Phe	Ser	Lys	Tyr	Tyr	Thr	Pro	Val	Leu	Ala
		675					680					685			
Lys	Ala	Val	Asp	Gly	Tyr	Val	Lys	Pro	Gln	Ile	Lys	Gln	Val	Val	Pro
	690					695					700				
Glu	Phe	Val	Asn	Ala	Ser	Ala	Asp	Ala	Gly	Gly	Ser	Ser	Ala	Thr	Tyr
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Met	Asp	Gln	Ala	Pro	Ser	Pro	Ala	Val	Cys	Pro	Gln	Ala	Pro	Tyr	Asn
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Met	Tyr	Pro	Gln	Asn	Pro	Asp	His	Val	Leu	Asp	Gln	Asp	Gly	Glu	Phe
			740					745					750		
Asp	Leu	Asp	Glu	Thr	Met	Asp	Val	Ala	Arg	His	Val	Glu	Glu	Leu	Leu
	755						760					765			
Arg	Arg	Pro	Met	Asp	Ser	Leu	Asp	Ser	Arg	Leu	Ser	Pro	Pro	Ala	Gly
	770					775					780				
Leu	Phe	Thr	Ser	Ala	Arg	Gly	Ser	Leu	Ser	Trp	Val	Pro	Arg	Ala	Arg
785					790					795					800
Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr
				805					810					815	
Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His
			820					825					830		
Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys
		835					840					845			
Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp
	850					855					860				
Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg
865					870					875					880
Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro
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Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn
			900					905					910		
Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn
		915					920					925			
Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu

930		935		940
Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met				
945		950		955
Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His				960
	965		970	975
Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn				
	980		985	990
Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu				
	995		1000	1005
Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp				
1010		1015		1020
His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu				
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20 25 30		
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc		144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35 40 45		
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc		192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50 55 60		
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag		240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys		
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Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85 90 95		
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag		336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		
100 105 110		

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
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Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
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Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
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Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
225 230 235 240	
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Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Met Pro Asp Pro	
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Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly Leu Phe Leu Leu	
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Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro Ala Glu Leu Cys	
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Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro Gly Val Phe Asp	
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Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg Gln Thr Trp Lys	
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Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg Met Pro Trp Tyr	
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Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val Tyr His Tyr Leu	
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465 470 475 480	
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Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys Leu Lys Ala Asp	
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Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala His Pro Ser Thr	
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Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met	
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Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu	
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625 630 635 640	
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Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val	
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Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe	
755 760 765	
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Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala	
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Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
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Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Met Pro Asp Pro  
245 250 255  
Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser Arg Ala Glu Ala  
260 265 270  
Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly Leu Phe Leu Leu  
275 280 285  
Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu Ser Leu Val His  
290 295 300  
Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln Leu Asn Gly Thr  
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Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro Ala Glu Leu Cys  
325 330 335  
Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys Asn Leu Arg Lys  
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Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro Gly Val Phe Asp  
355 360 365  
Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg Gln Thr Trp Lys  
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Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg Met Pro Trp Tyr  
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465 470 475 480  
Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys Leu Lys Ala Asp  
485 490 495  
Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn Ser Ser Ala Ser  
500 505 510  
Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala His Pro Ser Thr  
515 520 525  
Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn Ser Asp Gly Tyr  
530 535 540  
Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys Pro Arg Pro Met  
545 550 555 560  
Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu  
565 570 575  
Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala  
580 585 590  
Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val  
595 600 605  
Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys  
610 615 620  
Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln  
625 630 635 640  
Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val  
645 650 655  
Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met Ala Gly Gly Gly  
660 665 670  
Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser  
675 680 685  
Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly Met Lys Tyr Leu  
690 695 700  
Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Arg Asn Val Leu  
705 710 715 720  
Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys





Ile	Pro	Val	Ser	Asn	Val	Ala	Glu	Leu	Leu	His	Gln	Val	Ser	Met	Gly		
		435					440					445					
atg	aag	tac	ctg	gag	gag	aag	aac	ttt	gtg	cac	cgt	gac	ctg	gcg	gcc	1392	
Met	Lys	Tyr	Leu	Glu	Glu	Lys	Asn	Phe	Val	His	Arg	Asp	Leu	Ala	Ala		
		450					455					460					
cgc	aac	gtc	ctg	ctg	gtt	aac	cgg	cac	tac	gcc	aag	atc	agc	gac	ttt	1440	
Arg	Asn	Val	Leu	Leu	Val	Asn	Arg	His	Tyr	Ala	Lys	Ile	Ser	Asp	Phe		
		465				470				475					480		
ggc	ctc	tcc	aaa	gca	ctg	ggt	gcc	gac	gac	agc	tac	tac	act	gcc	cgc	1488	
Gly	Leu	Ser	Lys	Ala	Leu	Gly	Ala	Asp	Asp	Ser	Tyr	Tyr	Thr	Ala	Arg		
				485						490				495			
tca	gca	ggg	aag	tgg	ccg	ctc	aag	tgg	tac	gca	ccc	gaa	tgc	atc	aac	1536	
Ser	Ala	Gly	Lys	Trp	Pro	Leu	Lys	Trp	Tyr	Ala	Pro	Glu	Cys	Ile	Asn		
			500					505					510				
ttc	cgc	aag	ttc	tcc	agc	cgc	agc	gat	gtc	tgg	agc	tat	ggg	gtc	acc	1584	
Phe	Arg	Lys	Phe	Ser	Ser	Arg	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr		
		515					520					525					
atg	tgg	gag	gcc	ttg	tcc	tac	ggc	cag	aag	ccc	tac	aag	aag	atg	aaa	1632	
Met	Trp	Glu	Ala	Leu	Ser	Tyr	Gly	Gln	Lys	Pro	Tyr	Lys	Lys	Met	Lys		
		530				535				540							
ggg	ccg	gag	gtc	atg	gcc	ttc	atc	gag	cag	ggc	aag	cgg	atg	gag	tgc	1680	
Gly	Pro	Glu	Val	Met	Ala	Phe	Ile	Glu	Gln	Gly	Lys	Arg	Met	Glu	Cys		
					550					555					560		
cca	cca	gag	tgt	cca	ccc	gaa	ctg	tac	gca	ctc	atg	agt	gac	tgc	tgg	1728	
Pro	Pro	Glu	Cys	Pro	Pro	Glu	Leu	Tyr	Ala	Leu	Met	Ser	Asp	Cys	Trp		
				565				570						575			
atc	tac	aag	tgg	gag	gat	cgc	ccc	gac	ttc	ctg	acc	gtg	gag	cag	cgc	1776	
Ile	Tyr	Lys	Trp	Glu	Asp	Arg	Pro	Asp	Phe	Leu	Thr	Val	Glu	Gln	Arg		
			580					585					590				
atg	cga	gcc	tgt	tac	tac	agc	ctg	gcc	agc	aag	gtg	gaa	ggg	ccc	cca	1824	
Met	Arg	Ala	Cys	Tyr	Tyr	Ser	Leu	Ala	Ser	Lys	Val	Glu	Gly	Pro	Pro		
		595				600						605					
ggc	agc	aca	cag	aag	gct	gag	gct	gcc	tgt	gcc	tgg	gat	cca	ccg	gtc	1872	
Gly	Ser	Thr	Gln	Lys	Ala	Glu	Ala	Ala	Cys	Ala	Trp	Asp	Pro	Pro	Val		
		610				615					620						
gcc	acc	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	1920	
Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro		
		625			630					635					640		
atc	ctg	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	1968	
Ile	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val		
				645				650						655			
tcc	ggc	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	2016	
Ser	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys		
			660				665					670					
ttc	atc	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	2064	
Phe	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val		
		675				680						685					
acc	acc	ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	2112	
Thr	Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His		
		690			695					700							
atg	aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	2160	
Met	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val		
					710				715					720			
cag	gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	2208	
Gln	Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg		
				725				730						735			
gcc	gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	2256	
Ala	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu		
			740					745				750					
aag	ggc	atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	2304	
Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu		
		755					760					765					
gag	tac	aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	2352	

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
770 775 780	
aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	2400
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
785 790 795 800	
ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	2448
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
805 810 815	
gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc	2496
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser	
820 825 830	
gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	2544
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
835 840 845	
gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	2592
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
850 855 860	
aag taa	2598
Lys	
865	

<210> 111

<211> 865

<212> PRT

<213> Artificial Sequence

<220>

<223> Zap70-EGFP fusion

<400> 111

Met Pro Asp Pro Ala Ala His Leu Pro Phe Phe Tyr Gly Ser Ile Ser	
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Arg Ala Glu Ala Glu Glu His Leu Lys Leu Ala Gly Met Ala Asp Gly	
20 25 30	
Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu	
35 40 45	
Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln	
50 55 60	
Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro	
65 70 75 80	
Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys	
85 90 95	
Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro	
100 105 110	
Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg	
115 120 125	
Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser	
130 135 140	
Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg	
145 150 155 160	
Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys	
165 170 175	
Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg	
180 185 190	
Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val	

		195					200					205						
Tyr	His	Tyr	Leu	Ile	Ser	Gln	Asp	Lys	Ala	Gly	Lys	Tyr	Cys	Ile	Pro			
	210					215					220							
Glu	Gly	Thr	Lys	Phe	Asp	Thr	Leu	Trp	Gln	Leu	Val	Glu	Tyr	Leu	Lys			
225					230					235					240			
Leu	Lys	Ala	Asp	Gly	Leu	Ile	Tyr	Cys	Leu	Lys	Glu	Ala	Cys	Pro	Asn			
				245					250					255				
Ser	Ser	Ala	Ser	Asn	Ala	Ser	Gly	Ala	Ala	Ala	Pro	Thr	Leu	Pro	Ala			
				260				265					270					
His	Pro	Ser	Thr	Leu	Thr	His	Pro	Gln	Arg	Arg	Ile	Asp	Thr	Leu	Asn			
		275					280					285						
Ser	Asp	Gly	Tyr	Thr	Pro	Glu	Pro	Ala	Arg	Ile	Thr	Ser	Pro	Asp	Lys			
	290					295					300							
Pro	Arg	Pro	Met	Pro	Met	Asp	Thr	Ser	Val	Tyr	Glu	Ser	Pro	Tyr	Ser			
305					310					315					320			
Asp	Pro	Glu	Glu	Leu	Lys	Asp	Lys	Lys	Leu	Phe	Leu	Lys	Arg	Asp	Asn			
				325					330					335				
Leu	Leu	Ile	Ala	Asp	Ile	Glu	Leu	Gly	Cys	Gly	Asn	Phe	Gly	Ser	Val			
			340					345					350					
Arg	Gln	Gly	Val	Tyr	Arg	Met	Arg	Lys	Lys	Gln	Ile	Asp	Val	Ala	Ile			
		355					360					365						
Lys	Val	Leu	Lys	Gln	Gly	Thr	Glu	Lys	Ala	Asp	Thr	Glu	Glu	Met	Met			
	370					375					380							
Arg	Glu	Ala	Gln	Ile	Met	His	Gln	Leu	Asp	Asn	Pro	Tyr	Ile	Val	Arg			
385					390					395					400			
Leu	Ile	Gly	Val	Cys	Gln	Ala	Glu	Ala	Leu	Met	Leu	Val	Met	Glu	Met			
				405					410					415				
Ala	Gly	Gly	Gly	Pro	Leu	His	Lys	Phe	Leu	Val	Gly	Lys	Arg	Glu	Glu			
			420					425					430					
Ile	Pro	Val	Ser	Asn	Val	Ala	Glu	Leu	Leu	His	Gln	Val	Ser	Met	Gly			
		435					440					445						
Met	Lys	Tyr	Leu	Glu	Glu	Lys	Asn	Phe	Val	His	Arg	Asp	Leu	Ala	Ala			
	450					455					460							
Arg	Asn	Val	Leu	Leu	Val	Asn	Arg	His	Tyr	Ala	Lys	Ile	Ser	Asp	Phe			
465					470					475					480			
Gly	Leu	Ser	Lys	Ala	Leu	Gly	Ala	Asp	Asp	Ser	Tyr	Tyr	Thr	Ala	Arg			
				485					490					495				
Ser	Ala	Gly	Lys	Trp	Pro	Leu	Lys	Trp	Tyr	Ala	Pro	Glu	Cys	Ile	Asn			
			500					505					510					
Phe	Arg	Lys	Phe	Ser	Ser	Arg	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val	Thr			
		515					520					525						
Met	Trp</																	

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val  
 705 710 715 720  
 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg  
 725 730 735  
 Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu  
 740 745 750  
 Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu  
 755 760 765  
 Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln  
 770 775 780  
 Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp  
 785 790 795 800  
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly  
 805 810 815  
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser  
 820 825 830  
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu  
 835 840 845  
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr  
 850 855 860  
 Lys  
 865

<210> 112

<211> 1635

<212> DNA

<213> Artificial Sequence

<220>

<223> CDK2-EGFP fusion

<220>

<221> CDS

<222> (1)..(1632)

<400> 112  
 atg gag aac ttc caa aag gtg gaa aag atc gga gag ggc acg tac gga 48  
 Met Glu Asn Phe Gln Lys Val Glu Lys Ile Gly Glu Gly Thr Tyr Gly  
 1 5 10 15  
 gtt gtg tac aaa gcc aga aac aag ttg acg gga gag gtg gtg gcg ctt 96  
 Val Val Tyr Lys Ala Arg Asn Lys Leu Thr Gly Glu Val Val Ala Leu  
 20 25 30  
 aag aaa atc cgc ctg gac act gag act gag ggt gtg ccc agt act gcc 144  
 Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala  
 35 40 45  
 atc cga gag atc tct ctg ctt aag gag ctt aac cat cct aat att gtc 192  
 Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val  
 50 55 60  
 aag ctg ctg gat gtc att cac aca gaa aat aaa ctc tac ctg gtt ttt 240  
 Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe  
 65 70 75 80  
 gaa ttt ctg cac caa gat ctc aag aaa ttc atg gat gcc tct gct ctc 288



Glu	Phe	Leu	His	Gln	Asp	Leu	Lys	Lys	Phe	Met	Asp	Ala	Ser	Ala	Leu		
				85					90					95			
act	ggc	att	cct	ctt	ccc	ctc	atc	aag	agc	tat	ctg	ttc	cag	ctg	ctc		336
Thr	Gly	Ile	Pro	Leu	Pro	Leu	Ile	Lys	Ser	Tyr	Leu	Phe	Gln	Leu	Leu		
			100					105				110					
cag	ggc	cta	gct	ttc	tgc	cat	tct	cat	cgg	gtc	ctc	cac	cga	gac	ctt		384
Gln	Gly	Leu	Ala	Phe	Cys	His	Ser	His	Arg	Val	Leu	His	Arg	Asp	Leu		
		115					120				125						
aaa	cct	cag	aat	ctg	ctt	att	aac	aca	gag	ggg	gcc	atc	aag	cta	gca		432
Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asn	Thr	Glu	Gly	Ala	Ile	Lys	Leu	Ala		
		130				135					140						
gac	ttt	gga	cta	gcc	aga	gct	ttt	gga	gtc	cct	ggt	cgt	act	tac	acc		480
Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Val	Pro	Val	Arg	Thr	Tyr	Thr		
				145		150					155				160		
cat	gag	gtg	gtg	acc	ctg	tgg	tac	cga	gct	cct	gaa	atc	ctc	ctg	ggc		528
His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	Leu	Gly		
				165					170					175			
tcg	aaa	tat	tat	tcc	aca	gct	gtg	gac	atc	tgg	agc	ctg	ggc	tgc	atc		576
Ser	Lys	Tyr	Tyr	Ser	Thr	Ala	Val	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Ile		
			180					185				190					
ttt	gct	gag	atg	gtg	act	cgc	cgg	gcc	ctg	ttc	cct	gga	gat	tct	gag		624
Phe	Ala	Glu	Met	Val	Thr	Arg	Arg	Ala	Leu	Phe	Pro	Gly	Asp	Ser	Glu		
		195				200					205						
att	gac	cag	ctc	ttc	cgg	atc	ttt	cgg	act	ctg	ggg	acc	cca	gat	gag		672
Ile	Asp	Gln	Leu	Phe	Arg	Ile	Phe	Arg	Thr	Leu	Gly	Thr	Pro	Asp	Glu		
		210			215						220						
gtg	gtg	tgg	cca	gga	gtt	act	tct	atg	cct	gat	tac	aag	cca	agt	ttc		720
Val	Val	Trp	Pro	Gly	Val	Thr	Ser	Met	Pro	Asp	Tyr	Lys	Pro	Ser	Phe		
				225		230				235					240		
ccc	aag	tgg	gcc	cgg	caa	gat	ttt	agt	aaa	gtt	gta	cct	ccc	ctg	gat		768
Pro	Lys	Trp	Ala	Arg	Gln	Asp	Phe	Ser	Lys	Val	Val	Pro	Pro	Leu	Asp		
			245					250				255					
gaa	gat	gga	cgg	agg	ttg	tta	tcg	caa	atg	ctg	cac	tac	gac	cct	aac		816
Glu	Asp	Gly	Arg	Ser	Leu	Leu	Ser	Gln	Met	Leu	His	Tyr	Asp	Pro	Asn		
			260					265				270					
aag	cgg	att	tcg	gcc	aag	gca	gcc	ctg	gct	cac	cct	ttc	ttc	cag	gat		864
Lys	Arg	Ile	Ser	Ala	Lys	Ala	Ala	Leu	Ala	His	Pro	Phe	Phe	Gln	Asp		
		275				280					285						
gtg	acc	aag	cca	gta	ccc	cat	ctt	cga	ctc	tgg	gat	cca	ccg	gtc	gcc		912
Val	Thr	Lys	Pro	Val	Pro	His	Leu	Arg	Leu	Trp	Asp	Pro	Pro	Val	Ala		
		290				295					300						
acc	atg	gtg	agg	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc		960
Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile		
		305			310					315					320		
ctg	gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agg	gtg	tcc		1008
Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser		
			325					330				335					
ggc	gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc		1056
Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe		
			340					345				350					
atc	tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc		1104
Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr		
		355				360					365						
acc	ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agg	cgc	tac	ccc	gac	cac	atg		1152
Thr	Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met		
		370			375					380							
aag	cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag		1200
Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln		
		385			390				395						400		
gag	cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc		1248
Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala		
			405					410						415			
gag	gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag		1296

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys	
420 430	
ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag	1344
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu	
435 440 445	
tac aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	1392
Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
450 455 460	
aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc	1440
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly	
465 470 475 480	
agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	1488
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
485 490 495	
ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc	1536
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala	
500 505 510	
ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	1584
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
515 520 525	
ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	1632
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
530 535 540	
taa	1635

<210> 113

<211> 544

<212> PRT

<213> Artificial Sequence

<220>

<223> CDK2-EGFP fusion

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20 25 30	
Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu Gly Val Pro Ser Thr Ala	
35 40 45	
Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu Asn His Pro Asn Ile Val	
50 55 60	
Lys Leu Leu Asp Val Ile His Thr Glu Asn Lys Leu Tyr Leu Val Phe	
65 70 75 80	
Glu Phe Leu His Gln Asp Leu Lys Lys Phe Met Asp Ala Ser Ala Leu	
85 90 95	
Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser Tyr Leu Phe Gln Leu Leu	
100 105 110	
Gln Gly Leu Ala Phe Cys His Ser His Arg Val Leu His Arg Asp Leu	
115 120 125	
Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu Gly Ala Ile Lys Leu Ala	
130 135 140	
Asp Phe Gly Leu Ala Arg Ala Phe Gly Val Pro Val Arg Thr Tyr Thr	
145 150 155 160	
His Glu Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Ile Leu Leu Gly	



<220>

<221> CDS

<222> (1)..(1632)

<400> 114

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
			50			55					60					
ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
65				70					75					80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120						125			
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130			135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155				160		
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165				170					175			
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
			180				185						190			
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195			200						205				
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
			210			215					220					
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc	720
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
225					230					235				240		
gga	ctc	aga	tct	cga	gcc	atg	gag	aac	ttc	caa	aag	gtg	gaa	aag	atc	768
Gly	Leu	Arg	Ser	Arg	Ala	Met	Glu	Asn	Phe	Gln	Lys	Val	Glu	Lys	Ile	
				245					250					255		
gga	gag	ggc	acg	tac	gga	gtt	gtg	tac	aaa	gcc	aga	aac	aag	ttg	acg	816
Gly	Glu	Gly	Thr	Tyr	Gly	Val	Val	Tyr	Lys	Ala	Arg	Asn	Lys	Leu	Thr	
			260				265					270				
gga	gag	gtg	gtg	gcg	ctt	aag	aaa	atc	cgc	ctg	gac	act	gag	act	gag	864
Gly	Glu	Val	Val	Ala	Leu	Lys	Lys	Ile	Arg	Leu	Asp	Thr	Glu	Thr	Glu	
			275				280					285				

ggt gtc ccc agt act gcc atc cga gag atc tct ctg ctt aag gag ctt	912
Gly Val Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu	
290 295 300	
aac cat cct aat att gtc aag ctg ctg gat gtc att cac aca gaa aat	960
Asn His Pro Asn Ile Val Lys Leu Leu Asp Val Ile His Thr Glu Asn	
305 310 315 320	
aaa ctc tac ctg gtt ttt gaa ttt ctg cac caa gat ctc aag aaa ttc	1008
Lys Leu Tyr Leu Val Phe Glu Phe Leu His Gln Asp Leu Lys Lys Phe	
325 330 335	
atg gat gcc tct gct ctc act ggc att cct ctt ccc ctc atc aag agc	1056
Met Asp Ala Ser Ala Leu Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser	
340 345 350	
tat ctg ttc cag ctg ctc cag ggc cta gct ttc tgc cat tct cat cgg	1104
Tyr Leu Phe Gln Leu Leu Gln Gly Leu Ala Phe Cys His Ser His Arg	
355 360 365	
gtc ctc cac cga gac ctt aaa cct cag aat ctg ctt att aac aca gag	1152
Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu	
370 375 380	
ggg gcc atc aag cta gca gac ttt gga cta gcc aga gct ttt gga gtc	1200
Gly Ala Ile Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val	
385 390 395 400	
cct gtt cgt act tac acc cat gag gtg gtg acc ctg tgg tac cga gct	1248
Pro Val Arg Thr Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala	
405 410 415	
cct gaa atc ctc ctg ggc tcg aaa tat tat tcc aca gct gtg gac atc	1296
Pro Glu Ile Leu Leu Gly Ser Lys Tyr Tyr Ser Thr Ala Val Asp Ile	
420 425 430	
tgg agc ctg ggc tgc atc ttt gct gag atg gtg act cgc cgg gcc ctg	1344
Trp Ser Leu Gly Cys Ile Phe Ala Glu Met Val Thr Arg Arg Ala Leu	
435 440 445	
ttc cct gga gat tct gag att gac cag ctc ttc cgg atc ttt cgg act	1392
Phe Pro Gly Asp Ser Glu Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr	
450 455 460	
ctg ggg acc cca gat gag gtg gtg tgg cca gga gtt act tct atg cct	1440
Leu Gly Thr Pro Asp Glu Val Val Trp Pro Gly Val Thr Ser Met Pro	
465 470 475 480	
gat tac aag cca agt ttc ccc aag tgg gcc cgg caa gat ttt agt aaa	1488
Asp Tyr Lys Pro Ser Phe Pro Lys Trp Ala Arg Gln Asp Phe Ser Lys	
485 490 495	
gtt gta cct ccc ctg gat gaa gat gga cgg agc ttg tta tcg caa atg	1536
Val Val Pro Pro Leu Asp Glu Asp Gly Arg Ser Leu Leu Ser Gln Met	
500 505 510	
ctg cac tac gac cct aac aag cgg att tcg gcc aag gca gcc ctg gct	1584
Leu His Tyr Asp Pro Asn Lys Arg Ile Ser Ala Lys Ala Ala Leu Ala	
515 520 525	
cac cct ttc ttc cag gat gtg acc aag cca gta ccc cat ctt cga ctc	1632
His Pro Phe Phe Gln Asp Val Thr Lys Pro Val Pro His Leu Arg Leu	
530 535 540	
tga	1635

<210> 115

<211> 544

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-CDK2 fusion

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<400> 115
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20     25     30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35     40     45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50     55     60
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65     70     75     80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85     90     95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100    105    110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115    120    125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130    135    140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145    150    155    160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165    170    175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180    185    190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195    200    205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210    215    220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225    230    235    240
Gly Leu Arg Ser Arg Ala Met Glu Asn Phe Gln Lys Val Glu Lys Ile
245    250    255
Gly Glu Gly Thr Tyr Gly Val Val Tyr Lys Ala Arg Asn Lys Leu Thr
260    265    270
Gly Glu Val Val Ala Leu Lys Lys Ile Arg Leu Asp Thr Glu Thr Glu
275    280    285
Gly Val Pro Ser Thr Ala Ile Arg Glu Ile Ser Leu Leu Lys Glu Leu
290    295    300
Asn His Pro Asn Ile Val Lys Leu Leu Asp Val Ile His Thr Glu Asn
305    310    315    320
Lys Leu Tyr Leu Val Phe Glu Phe Leu His Gln Asp Leu Lys Lys Phe
325    330    335
Met Asp Ala Ser Ala Leu Thr Gly Ile Pro Leu Pro Leu Ile Lys Ser
340    345    350
Tyr Leu Phe Gln Leu Leu Gln Gly Leu Ala Phe Cys His Ser His Arg
355    360    365
Val Leu His Arg Asp Leu Lys Pro Gln Asn Leu Leu Ile Asn Thr Glu
370    375    380
Gly Ala Ile Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Gly Val
385    390    395    400
Pro Val Arg Thr Tyr Thr His Glu Val Val Thr Leu Trp Tyr Arg Ala
405    410    415
Pro Glu Ile Leu Leu Gly Ser Lys Tyr Tyr Ser Thr Ala Val Asp Ile
420    425    430
Trp Ser Leu Gly Cys Ile Phe Ala Glu Met Val Thr Arg Arg Ala Leu
435    440    445
Phe Pro Gly Asp Ser Glu Ile Asp Gln Leu Phe Arg Ile Phe Arg Thr
450    455    460
Leu Gly Thr Pro Asp Glu Val Val Trp Pro Gly Val Thr Ser Met Pro
465    470    475    480

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Asp	Tyr	Lys	Pro	Ser	Phe	Pro	Lys	Trp	Ala	Arg	Gln	Asp	Phe	Ser	Lys
				485					490					495	
Val	Val	Pro	Pro	Leu	Asp	Glu	Asp	Gly	Arg	Ser	Leu	Leu	Ser	Gln	Met
			500					505					510		
Leu	His	Tyr	Asp	Pro	Asn	Lys	Arg	Ile	Ser	Ala	Lys	Ala	Ala	Leu	Ala
		515					520					525			
His	Pro	Phe	Phe	Gln	Asp	Val	Thr	Lys	Pro	Val	Pro	His	Leu	Arg	Leu
	530					535					540				

<210> 116

<211> 2532

<212> DNA

<213> Artificial Sequence

<220>

<223> EGFP-PTP fusion

<220>

<221> CDS

<222> (1)..(2529)

<400>	116															
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Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50				55						60					
ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70				75					80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90						95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145				150					155					160	

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc	720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
225 230 235 240	
gga ctc aga tct cga gag atg ctg tcc cgt ggg tgg ttt cac cga gac	768
Gly Leu Arg Ser Arg Glu Met Leu Ser Arg Gly Trp Phe His Arg Asp	
245 250 255	
ctc agt ggg ctg gat gca gag acc ctg ctc aag ggc cga ggt gtc cac	816
Leu Ser Gly Leu Asp Ala Glu Thr Leu Lys Gly Arg Gly Val His	
260 265 270	
ggt agc ttc ctg gct cgg ccc agt cgc aag aac cag ggt gac ttc tcg	864
Gly Ser Phe Leu Ala Arg Pro Ser Arg Lys Asn Gln Gly Asp Phe Ser	
275 280 285	
ctc tcc gtc agg gtg ggg gat cag gtg acc cat att cgg atc cag aac	912
Leu Ser Val Arg Val Gly Asp Gln Val Thr His Ile Arg Ile Gln Asn	
290 295 300	
tca ggg gat ttc tat gac ctg tat gga ggg gag aag ttt gcg act ctg	960
Ser Gly Asp Phe Tyr Asp Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu	
305 310 315 320	
aca gag ctg gtg gag tac tac act cag cag cag ggt gtc ctg cag gac	1008
Thr Glu Leu Val Glu Tyr Tyr Thr Gln Gln Gly Val Leu Gln Asp	
325 330 335	
cgc gac ggc acc atc atc cac ctc aag tac ccg ctg aac tgc tcc gat	1056
Arg Asp Gly Thr Ile Ile His Leu Lys Tyr Pro Leu Asn Cys Ser Asp	
340 345 350	
ccc act agt gag agg tgg tac cat ggc cac atg tct ggc ggg cag gca	1104
Pro Thr Ser Glu Arg Trp Tyr His Gly His Met Ser Gly Gly Gln Ala	
355 360 365	
gag acg ctg ctg cag gcc aag ggc gag ccc tgg acg ttt ctt gtg cgt	1152
Glu Thr Leu Leu Gln Ala Lys Gly Glu Pro Trp Thr Phe Leu Val Arg	
370 375 380	
gag agc ctc agc cag cct gga gac ttc gtg ctt tct gtg ctc agt gac	1200
Glu Ser Leu Ser Gln Pro Gly Asp Phe Val Leu Ser Val Leu Ser Asp	
385 390 395 400	
cag ccc aag gct ggc cca ggc tcc ccg ctc agg gtc acc cac atc aag	1248
Gln Pro Lys Ala Gly Pro Gly Ser Pro Leu Arg Val Thr His Ile Lys	
405 410 415	
gtc atg tgc gag ggt gga cgc tac aca gtg ggt ggt ttg gag acc ttc	1296
Val Met Cys Glu Gly Gly Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe	
420 425 430	
gac agc ctc acg gac ctg gta gag cat ttc aag aag acg ggg att gag	1344
Asp Ser Leu Thr Asp Leu Val Glu His Phe Lys Lys Thr Gly Ile Glu	
435 440 445	
gag gcc tca ggc gcc ttt gtc tac ctg cgg cag ccg tac tat gcc acg	1392
Glu Ala Ser Gly Ala Phe Val Tyr Leu Arg Gln Pro Tyr Tyr Ala Thr	
450 455 460	
agg gtg aat gcg gct gac att gag aac cga gtg ttg gaa ctg aac aag	1440
Arg Val Asn Ala Ala Asp Ile Glu Asn Arg Val Leu Glu Leu Asn Lys	
465 470 475 480	
aag cag gag tcc gag gat aca gcc aag gct ggc ttc tgg gag gag ttt	1488
Lys Gln Glu Ser Glu Asp Thr Ala Lys Ala Gly Phe Trp Glu Glu Phe	
485 490 495	



gag agt ttg cag aag cag gag gtg aag aac ttg cac cag cgt ctg gaa	1536
Glu Ser Leu 500 Gln Lys Gln Glu Val 505 Lys Asn Leu His Gln Arg Leu Glu 510	
ggg cag cgg cca gag aac aag ggc aag aac cgc tac aag aac att ctc	1584
Gly Gln Arg Pro Glu Asn Lys Gly Lys Asn Arg Tyr Lys Asn Ile Leu 515 520 525	
ccc ttt gac cac agc cga gtg atc ctg cag gga cgg gac agt aac atc	1632
Pro Phe Asp His Ser Arg Val 535 Ile Leu Gln Gly 540 Arg Asp Ser Asn Ile 530	
ccc ggg tcc gac tac atc aat gcc aac tac atc aag aac cag ctg cta	1680
Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Lys Asn Gln Leu Leu 545 550 555 560	
ggc cct gat gag aac gct aag acc tac atc gcc agc cag ggc tgt ctg	1728
Gly Pro Asp Glu Asn Ala Lys Thr Tyr 570 Ile Ala Ser Gln Gly Cys Leu 565 575	
gag gcc acg gtc aat gac ttc tgg cag atg gcg tgg cag gag aac agc	1776
Glu Ala Thr Val Asn Asp Phe Trp Gln Met Ala Trp Gln Glu Asn Ser 580 585 590	
cgt gtc atc gtc atg acc acc cga gag gtg gag aaa ggc cgg aac aaa	1824
Arg Val Ile Val Met Thr Thr Arg Glu Val Glu Lys Gly Arg Asn Lys 595 600 605	
tgc gtc cca tac tgg ccc gag gtg ggc atg cag cgt gct tat ggg ccc	1872
Cys Val Pro Tyr Trp Pro Glu Val Gly Met Gln Arg Ala Tyr Gly Pro 610 615 620	
tac tct gtg acc aac tgc ggg gag cat gac aca acc gaa tac aaa ctc	1920
Tyr Ser Val Thr Asn Cys Gly Glu His Asp Thr Thr Glu Tyr Lys Leu 625 630 635 640	
cgt acc tta cag gtc tcc ccg ctg gac aat gga gac ctg att cgg gag	1968
Arg Thr Leu Gln Val Ser Pro Leu Asp Asn Gly Asp Leu Ile Arg Glu 645 650 655	
atc tgg cat tac cag tac ctg agc tgg ccc gac cat ggg gtc ccc agt	2016
Ile Trp His 660 Gln Tyr Leu Ser Trp Pro Asp His Gly Val Pro Ser 665 670	
gag cct ggg ggt gtc ctc agc ttc ctg gac cag atc aac cag cgg cag	2064
Glu Pro Gly Gly Val Leu Ser Phe Leu Asp Gln Ile Asn Gln Arg Gln 675 680 685	
gaa agt ctg cct cac gca ggg ccc atc atc gtg cac tgc agc gcc ggc	2112
Glu Ser Leu Pro His Ala Gly Pro Ile Ile Val His Cys Ser Ala Gly 690 695 700	
atc ggc cgc aca ggc acc atc att gtc atc gac atg ctc atg gag aac	2160
Ile Gly Arg Thr Gly Thr Ile Ile Val Ile Asp Met Leu Met Glu Asn 705 710 715 720	
atc tcc acc aag ggc ctg gac tgt gac att gac atc cag aag acc atc	2208
Ile Ser Thr Lys Gly Leu Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile 725 730 735	
cag atg gtg cgg gcg cag cgc tcg ggc atg gtg cag acg gag gcg cag	2256
Gln Met Val Arg Ala Gln Arg Ser Gly Met Val Gln Thr Glu Ala Gln 740 745 750	
tac aag ttc atc tac gtg gcc atc gcc cag ttc att gaa acc act aag	2304
Tyr Lys Phe Ile Tyr Val Ala Ile Ala Gln Phe Ile Glu Thr Thr Lys 755 760 765	
aag aag ctg gag gtc ctg cag tcg cag aag ggc cag gag tcg gag tac	2352
Lys Lys Leu Glu Val Leu Gln Ser Gln Lys Gly Gln Glu Ser Glu Tyr 770 775 780	
ggg aac atc acc tat ccc cca gcc atg aag aat gcc cat gcc aag gcc	2400
Gly Asn Ile Thr Tyr Pro Ala Met Lys Asn Ala His Ala Lys Ala 785 790 795 800	
tcc cgc acc tcg tcc aaa cac aag gag gat gtg tat gag aac ctg cac	2448
Ser Arg Thr Ser Ser Lys His Lys Glu Asp Val Tyr Glu Asn Leu His 805 810 815	
act aag aac aag agg gag gag aaa gtg aag aag cag cgg tca gca gac	2496
Thr Lys Asn 820 Arg Glu Glu Lys 825 Val Lys Lys Gln Arg Ser Ala Asp 830	



Pro	Thr	Ser	Glu	Arg	Trp	Tyr	His	Gly	His	Met	Ser	Gly	Gly	Gln	Ala		
		355					360					365					
Glu	Thr	Leu	Leu	Gln	Ala	Lys	Gly	Glu	Pro	Trp	Thr	Phe	Leu	Val	Arg		
	370					375					380						
Glu	Ser	Leu	Ser	Gln	Pro	Gly	Asp	Phe	Val	Leu	Ser	Val	Leu	Ser	Asp		
385					390					395					400		
Gln	Pro	Lys	Ala	Gly	Pro	Gly	Ser	Pro	Leu	Arg	Val	Thr	His	Ile	Lys		
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Val	Met	Cys	Glu	Gly	Gly	Arg	Tyr	Thr	Val	Gly	Gly	Leu	Glu	Thr	Phe		
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Asp	Ser	Leu	Thr	Asp	Leu	Val	Glu	His	Phe	Lys	Lys	Thr	Gly	Ile	Glu		
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Glu	Ala	Ser	Gly	Ala	Phe	Val	Tyr	Leu	Arg	Gln	Pro	Tyr	Tyr	Ala	Thr		
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Arg	Val	Asn	Ala	Ala	Asp	Ile	Glu	Asn	Arg	Val	Leu	Glu	Leu	Asn	Lys		
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Glu	Ser	Leu	Gln	Lys	Gln	Glu	Val	Lys	Asn	Leu	His	Gln	Arg	Leu	Glu		
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Gly	Gln	Arg	Pro	Glu	Asn	Lys	Gly	Lys	Asn	Arg	Tyr	Lys	Asn	Ile	Leu		
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Pro	Gly	Ser	Asp	Tyr	Ile	Asn	Ala	Asn	Tyr	Ile	Lys	Asn	Gln	Leu	Leu		
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Gly	Pro	Asp	Glu	Asn	Ala	Lys	Thr	Tyr	Ile	Ala	Ser	Gln	Gly	Cys	Leu		
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Glu	Ala	Thr	Val	Asn	Asp	Phe	Trp	Gln	Met	Ala	Trp	Gln	Glu	Asn	Ser		
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Arg	Val	Ile	Val	Met	Thr	Thr	Arg	Glu	Val	Glu	Lys	Gly	Arg	Asn	Lys		
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Cys	Val	Pro	Tyr	Trp	Pro	Glu	Val	Gly	Met	Gln	Arg	Ala	Tyr	Gly	Pro		
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Tyr	Ser	Val	Thr	Asn	Cys	Gly	Glu	His	Asp	Thr	Thr	Glu	Tyr	Lys	Leu		
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Arg	Thr	Leu	Gln	Val	Ser	Pro	Leu	Asp	Asn	Gly	Asp	Leu	Ile	Arg	Glu		
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Glu	Pro	Gly	Gly	Val	Leu	Ser	Phe	Leu	Asp	Gln	Ile	Asn	Gln	Arg	Gln		
		675					680					685					
Glu	Ser	Leu	Pro	His	Ala	Gly	Pro	Ile	Ile	Val	His	Cys	Ser	Ala	Gly		
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Ile	Ser	Thr	Lys	Gly	Leu	Asp	Cys	Asp	Ile	Asp	Ile	Gln	Lys	Thr	Ile		
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Gln	Met	Val	Arg	Ala	Gln	Arg	Ser	Gly	Met	Val	Gln	Thr	Glu	Ala	Gln		
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Tyr	Lys	Phe	Ile	Tyr	Val	Ala	Ile	Ala	Gln	Phe	Ile	Glu	Thr	Thr	Lys		
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Lys	Lys	Leu	Glu	Val	Leu	Gln	Ser	Gln	Lys	Gly	Gln	Glu	Ser	Glu	Tyr		
	770					775					780						
Gly	Asn	Ile	Thr	Tyr	Pro	Pro	Ala	Met	Lys	Asn	Ala	His	Ala	Lys	Ala		
785					790					795					800		
Ser	Arg	Thr	Ser	Ser	Lys	His	Lys	Glu	Asp	Val	Tyr	Glu	Asn	Leu	His		
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Lys	Glu	Lys	Ser	Lys	Gly	Ser	Leu	Lys	Arg	Lys							
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 gag acc ctg ctc aag ggc cga ggt gtc cac ggt agc ttc ctg gct cgg 96  
 Glu Thr Leu Leu Lys Gly Arg Gly Val His Gly Ser Phe Leu Ala Arg  
 20 25 30  
 ccc agt cgc aag aac cag ggt gac ttc tcg ctc tcc gtc agg gtg ggg 144  
 Pro Ser Arg Lys Asn Gln Gly Asp Phe Ser Leu Ser Val Arg Val Gly  
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 gat cag gtg acc cat att cgg atc cag aac tca ggg gat ttc tat gac 192  
 Asp Gln Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp  
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 ctg tat gga ggg gag aag ttt gcg act ctg aca gag ctg gtg gag tac 240  
 Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr  
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 tac act cag cag cag ggt gtc ctg cag gac cgc gac ggc acc atc atc 288  
 Tyr Thr Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile  
 85 90 95  
 cac ctc aag tac ccg ctg aac tgc tcc gat ccc act agt gag agg tgg 336  
 His Leu Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp  
 100 105 110  
 tac cat ggc cac atg tct ggc ggg cag gca gag acg ctg ctg cag gcc 384  
 Tyr His Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala  
 115 120 125  
 aag ggc gag ccc tgg acg ttt ctt gtg cgt gag agc ctc agc cag cct 432  
 Lys Gly Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro  
 130 135 140  
 gga gac ttc gtg ctt tct gtg ctc agt gac cag ccc aag gct ggc cca 480  
 Gly Asp Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro  
 145 150 155 160  
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 Gly Ser Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly  
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 cgc tac aca gtg ggt ggt ttg gag acc ttc gac agc ctc acg gac ctg 576  
 Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu  
 180 185 190  
 gta gag cat ttc aag aag acg ggg att gag gag gcc tca gcc ttt 624  
 Val Glu His Phe Lys Lys Thr Gly Ile Glu Glu Ala Ser Gly Ala Phe

gtc	tac	ctg	cgg	cag	ccg	tac	tat	gcc	acg	agg	gtg	aat	gcg	gct	gac	672
Val	Tyr	Leu	Arg	Gln	Pro	Tyr	Tyr	Ala	Thr	Arg	Val	Asn	Ala	Ala	Asp	
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Ile	Glu	Asn	Arg	Val	Leu	Glu	Leu	Asn	Lys	Lys	Gln	Glu	Ser	Glu	Asp	
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Thr	Ala	Lys	Ala	Gly	Phe	Trp	Glu	Glu	Phe	Glu	Ser	Leu	Gln	Lys	Gln	
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Glu	Val	Lys	Asn	Leu	His	Gln	Arg	Leu	Glu	Gly	Gln	Arg	Pro	Glu	Asn	
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Lys	Gly	Lys	Asn	Arg	Tyr	Lys	Asn	Ile	Leu	Pro	Phe	Asp	His	Ser	Arg	
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Val	Ile	Leu	Gln	Gly	Arg	Asp	Ser	Asn	Ile	Pro	Gly	Ser	Asp	Tyr	Ile	
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Asn	Ala	Asn	Tyr	Ile	Lys	Asn	Gln	Leu	Leu	Gly	Pro	Asp	Glu	Asn	Ala	
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Lys	Thr	Tyr	Ile	Ala	Ser	Gln	Gly	Cys	Leu	Glu	Ala	Thr	Val	Asn	Asp	
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Phe	Trp	Gln	Met	Ala	Trp	Gln	Glu	Asn	Ser	Arg	Val	Ile	Val	Met	Thr	
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Thr	Arg	Glu	Val	Glu	Lys	Gly	Arg	Asn	Lys	Cys	Val	Pro	Tyr	Trp	Pro	
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Glu	Val	Gly	Met	Gln	Arg	Ala	Tyr	Gly	Pro	Tyr	Ser	Val	Thr	Asn	Cys	
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Gly	Glu	His	Asp	Thr	Thr	Glu	Tyr	Lys	Leu	Arg	Thr	Leu	Gln	Val	Ser	
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ccg	ctg	gac	aat	gga	gac	ctg	att	cgg	gag	atc	tgg	cat	tac	cag	tac	1248
Pro	Leu	Asp	Asn	Gly	Asp	Leu	Ile	Arg	Glu	Ile	Trp	His	Tyr	Gln	Tyr	
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Leu	Ser	Trp	Pro	Asp	His	Gly	Val	Pro	Ser	Glu	Pro	Gly	Gly	Val	Leu	
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Ser	Phe	Leu	Asp	Gln	Ile	Asn	Gln	Arg	Gln	Glu	Ser	Leu	Pro	His	Ala	
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Gly	Pro	Ile	Ile	Val	His	Cys	Ser	Ala	Gly	Ile	Gly	Arg	Thr	Gly	Thr	
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Ile	Ile	Val	Ile	Asp	Met	Leu	Met	Glu	Asn	Ile	Ser	Thr	Lys	Gly	Leu	
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Asp	Cys	Asp	Ile	Asp	Ile	Gln	Lys	Thr	Ile	Gln	Met	Val	Arg	Ala	Gln	
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Arg	Ser	Gly	Met	Val	Gln	Thr	Glu	Ala	Gln	Tyr	Lys	Phe	Ile	Tyr	Val	
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Ala	Ile	Ala	Gln	Phe	Ile	Glu	Thr	Thr	Lys	Lys	Lys	Leu	Glu	Val	Leu	
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Gln	Ser	Gln	Lys	Gly	Gln	Glu	Ser	Glu	Tyr	Gly	Asn	Ile	Thr	Tyr	Pro	
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Pro Ala Met Lys Asn Ala His Ala Lys Ala Ser Arg Thr Ser Lys			
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cac aag gag gat gtg tat gag aac ctg cac act aag aac aag agg gag			1728
His Lys Glu Asp Val Tyr Glu Asn Leu His Thr Lys Asn Lys Arg Glu			
565	570	575	
gag aaa gtg aag aag cag cgg tca gca gac aag gag aag agc aag ggt			1776
Glu Lys Val Lys Lys Gln Arg Ser Ala Asp Lys Glu Lys Ser Lys Gly			
580	585	590	
tcc ctc aag agg aag cga att ctg cag tcg acg gta ccg cgg gcc cgg			1824
Ser Leu Lys Arg Lys Arg Ile Leu Gln Ser Thr Val Pro Arg Ala Arg			
595	600	605	
gat cca ccg gtc gcc acc atg gtg agc aag ggc gag gag ctg ttc acc			1872
Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr			
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ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac			1920
Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His			
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aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag			1968
Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys			
645	650	655	
ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg			2016
Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp			
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ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag tgc ttc agc cgc			2064
Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg			
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Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro			
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Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn			
705	710	715	720
tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac			2208
Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn			
725	730	735	
cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg			2256
Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu			
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Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met			
755	760	765	
gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac			2352
Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His			
770	775	780	
aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac			2400
Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn			
785	790	795	800
acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg			2448
Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu			
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Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His			
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<212> PRT

<213> Artificial Sequence

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<223> PTP-EGFP fusion

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      35      40      45
Asp Gln Val Thr His Ile Arg Ile Gln Asn Ser Gly Asp Phe Tyr Asp
      50      55      60
Leu Tyr Gly Gly Glu Lys Phe Ala Thr Leu Thr Glu Leu Val Glu Tyr
      65      70      75      80
Tyr Thr Gln Gln Gln Gly Val Leu Gln Asp Arg Asp Gly Thr Ile Ile
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His Leu Lys Tyr Pro Leu Asn Cys Ser Asp Pro Thr Ser Glu Arg Trp
      100      105      110
Tyr His Gly His Met Ser Gly Gly Gln Ala Glu Thr Leu Leu Gln Ala
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Lys Gly Glu Pro Trp Thr Phe Leu Val Arg Glu Ser Leu Ser Gln Pro
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Gly Asp Phe Val Leu Ser Val Leu Ser Asp Gln Pro Lys Ala Gly Pro
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Gly Ser Pro Leu Arg Val Thr His Ile Lys Val Met Cys Glu Gly Gly
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Arg Tyr Thr Val Gly Gly Leu Glu Thr Phe Asp Ser Leu Thr Asp Leu
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      195      200      205
Val Tyr Leu Arg Gln Pro Tyr Tyr Ala Thr Arg Val Asn Ala Ala Asp
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Ile Glu Asn Arg Val Leu Glu Leu Asn Lys Lys Gln Glu Ser Glu Asp
      225      230      235      240
Thr Ala Lys Ala Gly Phe Trp Glu Glu Phe Glu Ser Leu Gln Lys Gln
      245      250      255
Glu Val Lys Asn Leu His Gln Arg Leu Glu Gly Gln Arg Pro Glu Asn
      260      265      270
Lys Gly Lys Asn Arg Tyr Lys Asn Ile Leu Pro Phe Asp His Ser Arg
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Val Ile Leu Gln Gly Arg Asp Ser Asn Ile Pro Gly Ser Asp Tyr Ile
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Asn Ala Asn Tyr Ile Lys Asn Gln Leu Leu Gly Pro Asp Glu Asn Ala
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Lys Thr Tyr Ile Ala Ser Gln Gly Cys Leu Glu Ala Thr Val Asn Asp
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Phe Trp Gln Met Ala Trp Gln Glu Asn Ser Arg Val Ile Val Met Thr
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Glu Val Gly Met Gln Arg Ala Tyr Gly Pro Tyr Ser Val Thr Asn Cys
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 Leu Ser Trp Pro Asp His Gly Val Pro Ser Glu Pro Gly Gly Val Leu  
 420 425 430  
 Ser Phe Leu Asp Gln Ile Asn Gln Arg Gln Glu Ser Leu Pro His Ala  
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 Gly Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr  
 450 455 460  
 Ile Ile Val Ile Asp Met Leu Met Glu Asn Ile Ser Thr Lys Gly Leu  
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 Asp Cys Asp Ile Asp Ile Gln Lys Thr Ile Gln Met Val Arg Ala Gln  
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 Arg Ser Gly Met Val Gln Thr Glu Ala Gln Tyr Lys Phe Ile Tyr Val  
 500 505 510  
 Ala Ile Ala Gln Phe Ile Glu Thr Lys Lys Lys Leu Glu Val Leu  
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 Pro Ala Met Lys Asn Ala His Ala Lys Ala Ser Arg Thr Ser Ser Lys  
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 His Lys Glu Asp Val Tyr Glu Asn Leu His Thr Lys Asn Lys Arg Glu  
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 Glu Lys Val Lys Lys Gln Arg Ser Ala Asp Lys Glu Lys Ser Lys Gly  
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 595 600 605  
 Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr  
 610 615 620  
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His  
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 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys  
 645 650 655  
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp  
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 Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg  
 675 680 685  
 Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro  
 690 695 700  
 Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn  
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 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn  
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 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met  
 755 760 765  
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His  
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 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn  
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 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu  
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 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His  
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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20          25          30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35          40          45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50          55          60
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag      240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65          70          75          80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85          90          95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100          105          110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115          120          125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130          135          140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145          150          155          160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165          170          175
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc      576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180          185          190
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg      624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195          200          205
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc      672

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Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Asn	Ser	Thr	Met	Glu	Arg	Pro		
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Pro	Gly	Leu	Arg	Pro	Gly	Ala	Gly	Gly	Pro	Trp	Glu	Met	Arg	Glu	Arg		
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Leu	Gly	Thr	Gly	Gly	Phe	Gly	Asn	Val	Cys	Leu	Tyr	Gln	His	Arg	Glu		
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ctt	gat	ctc	aaa	ata	gca	att	aag	tct	tgt	cgc	cta	gag	cta	agt	acc		912
Leu	Asp	Leu	Lys	Ile	Ala	Ile	Lys	Ser	Cys	Arg	Leu	Glu	Leu	Ser	Thr		
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Asn	His	Ala	Asn	Val	Val	Lys	Ala	Cys	Asp	Val	Pro	Glu	Glu	Leu	Asn		
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att	ttg	att	cat	gat	gtg	cct	ctt	cta	gca	atg	gaa	tac	tgt	tct	gga		1056
Ile	Leu	Ile	His	Asp	Val	Pro	Leu	Leu	Ala	Met	Glu	Tyr	Cys	Ser	Gly		
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aaa	gaa	agc	cag	ata	ctt	tct	tta	cta	agt	gat	ata	ggg	tct	ggg	att		1152
Lys	Glu	Ser	Gln	Ile	Leu	Ser	Leu	Leu	Ser	Asp	Ile	Gly	Ser	Gly	Ile		
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Asn	Ile	Val	Leu	Gln	Asp	Val	Gly	Gly	Lys	Ile	Ile	His	Lys	Ile	Ile		
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gat	ctg	gga	tat	gcc	aaa	gat	gtt	gat	caa	gga	agt	ctg	tgt	aca	tct		1296
Asp	Leu	Gly	Tyr	Ala	Lys	Asp	Val	Asp	Gln	Gly	Ser	Leu	Cys	Thr	Ser		
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ttt	gtg	gga	aca	ctg	cag	tat	ctg	gcc	cca	gag	ctc	ttt	gag	aat	aag		1344
Phe	Val	Gly	Thr	Leu	Gln	Tyr	Leu	Ala	Pro	Glu	Leu	Phe	Glu	Asn	Lys		
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cct	tac	aca	gcc	act	gtt	gat	tat	tgg	agc	ttt	ggg	acc	atg	gta	ttt		1392
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gaa	tgt	att	gct	gga	tat	agg	cct	ttt	ttg	cat	cat	ctg	cag	cca	ttt		1440
Glu	Cys	Ile	Ala	Gly	Tyr	Arg	Pro	Phe	Leu	His	His	Leu	Gln	Pro	Phe		
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acc	tgg	cat	gag	aag	att	aag	aag	aag	gat	cca	aag	tgt	ata	ttt	gca		1488
Thr	Trp	His	Glu	Lys	Ile	Lys	Lys	Lys	Asp	Pro	Lys	Cys	Ile	Phe	Ala		
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Cys	Glu	Glu	Met	Ser	Gly	Glu	Val	Arg	Phe	Ser	Ser	His	Leu	Pro	Gln		
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Pro	Asn	Ser	Leu	Cys	Ser	Leu	Ile	Val	Glu	Pro	Met	Glu	Asn	Trp	Leu		
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Gln	Leu	Met	Leu	Asn	Trp	Asp	Pro	Gln	Gln	Arg	Gly	Gly	Pro	Val	Asp		
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ctt	act	ttg	aag	cag	cca	aga	tgt	ttt	gta	tta	atg	gat	cac	att	ttg		1680

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Asn Leu Lys Ile Val His Ile Leu Asn Met Thr Ser Ala Lys Ile Ile	
565 570 575	
tct ttt ctg tta cca cct gat gaa agt ctt cat tca cta cag tct cgt	1776
Ser Phe Leu Leu Pro Pro Asp Glu Ser Leu His Ser Leu Gln Ser Arg	
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Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln Glu Leu Leu Ser	
595 600 605	
gag aca gga att tct ctg gat cct cgg aaa cca gcc tct caa tgt gtt	1872
Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala Ser Gln Cys Val	
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cta gat gga gtt aga ggc tgt gat agc tat atg gtt tat ttg ttt gat	1920
Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val Tyr Leu Phe Asp	
625 630 635 640	
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Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser Arg Ser Leu Ser	
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Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile Gln Leu Pro Ile	
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Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His Tyr Val Ser Gly	
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Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln Arg Ala Ala Met	
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Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu Gln Met Thr Tyr	
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755 760 765	
aag gcc atc cac tat gct gag gtt ggt gtc att gga tac ctg gag gat	2352
Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly Tyr Leu Glu Asp	
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Gln Ile Met Ser Leu His Ala Glu Ile Met Gly Leu Gln Lys Ser Pro	
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Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu Glu Gln Arg Ala	
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Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His Thr Val Gln Ser	
835 840 845	
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Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu Ser Lys Leu Leu	
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Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys Val Glu Val Ala	
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Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
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Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
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Phe	Val	Gly	Thr	Leu	Gln	Tyr	Leu	Ala	Pro	Glu	Leu	Phe	Glu	Asn	Lys
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Thr	Trp	His	Glu	Lys	Ile	Lys	Lys	Lys	Asp	Pro	Lys	Cys	Ile	Phe	Ala
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Lys	Ser	Lys	Thr	Val	Tyr	Glu	Gly	Pro	Phe	Ala	Ser	Arg	Ser	Leu	Ser
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Asp	Cys	Val	Asn	Tyr	Ile	Val	Gln	Asp	Ser	Lys	Ile	Gln	Leu	Pro	Ile
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Lys	Ala	Ile	His	Tyr	Ala	Glu	Val	Gly	Val	Ile	Gly	Tyr	Leu	Glu	Asp
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Tyr	Gly	Arg	Arg	Gln	Gly	Asp	Leu	Met	Glu	Ser	Leu	Glu	Gln	Arg	Ala
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865					870					875					880
Leu	Ser	Asn	Ile	Lys	Glu	Ala	Asp	Asn	Thr	Val	Met	Phe	Met	Gln	Gly
				885					890					895	
Lys	Arg	Gln	Lys	Glu	Ile	Trp	His	Leu	Leu	Lys	Ile	Ala	Cys	Thr	Gln
		900						905					910		
Ser	Ser	Ala	Arg	Ser	Leu	Val	Gly	Ser	Ser	Leu	Glu	Gly	Ala	Val	Thr
		915					920					925			
Pro	Gln	Thr	Ser	Ala	Trp	Leu	Pro	Pro	Thr	Ser	Ala	Glu	His	Asp	His
		930				935						940			
Ser	Leu	Ser	Cys	Val	Val	Thr	Pro	Gln	Asp	Gly	Glu	Thr	Ser	Ala	Gln
945					950					955					960
Met	Ile	Glu	Glu	Asn	Leu	Asn	Cys	Leu	Gly	His	Leu	Ser	Thr	Ile	Ile
				965					970					975	
His	Glu	Ala	Asn	Glu	Glu	Gln	Gly	Asn	Ser	Met	Met	Asn	Leu	Asp	Trp
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Ser	Trp	Leu	Thr	Glu											
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<210> 122

<211> 2991

<212> DNA

<213> Artificial Sequence

<220>

<223> IkappaB-kinase-EGFP fusion

<220>

<221> CDS

<222> (1)..(2988)



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Ala Lys Ile Ile Ser Phe Leu Leu Pro Asp Glu Ser Leu His Ser	
325 330 335	
cta cag tct cgt att gag cgt gaa act gga ata aat act ggt tct caa	1056
Leu Gln Ser Arg Ile Glu Arg Glu Thr Gly Ile Asn Thr Gly Ser Gln	
340 345 350	
gaa ctt ctt tca gag aca gga att tct ctg gat cct cgg aaa cca gcc	1104
Glu Leu Leu Ser Glu Thr Gly Ile Ser Leu Asp Pro Arg Lys Pro Ala	
355 360 365	
tct caa tgt gtt cta gat gga gtt aga ggc tgt gat agc tat atg gtt	1152
Ser Gln Cys Val Leu Asp Gly Val Arg Gly Cys Asp Ser Tyr Met Val	
370 375 380	
tat ttg ttt gat aaa agt aaa act gta tat gaa ggg cca ttt gct tcc	1200
Tyr Leu Phe Asp Lys Ser Lys Thr Val Tyr Glu Gly Pro Phe Ala Ser	
385 390 395 400	
aga agt tta tct gat tgt gta aat tat att gta cag gac agc aaa ata	1248
Arg Ser Leu Ser Asp Cys Val Asn Tyr Ile Val Gln Asp Ser Lys Ile	
405 410 415	
cag ctt cca att ata cag ctg cgt aaa gtg tgg gct gaa gca gtg cac	1296
Gln Leu Pro Ile Ile Gln Leu Arg Lys Val Trp Ala Glu Ala Val His	
420 425 430	
tat gtg tct gga cta aaa gaa gac tat agc agg ctc ttt cag gga caa	1344
Tyr Val Ser Gly Leu Lys Glu Asp Tyr Ser Arg Leu Phe Gln Gly Gln	
435 440 445	
agg gca gca atg tta agt ctt ctt aga tat aat gct aac tta aca aaa	1392
Arg Ala Ala Met Leu Ser Leu Leu Arg Tyr Asn Ala Asn Leu Thr Lys	
450 455 460	
atg aag aac act ttg atc tca gca tca caa caa ctg aaa gct aaa ttg	1440
Met Lys Asn Thr Leu Ile Ser Ala Ser Gln Gln Leu Lys Ala Lys Leu	
465 470 475 480	
gag ttt ttt cac aaa agc att cag ctt gac ttg gag aga tac agc gag	1488
Glu Phe Phe His Lys Ser Ile Gln Leu Asp Leu Glu Arg Tyr Ser Glu	
485 490 495	
cag atg acg tat ggg ata tct tca gaa aaa atg cta aaa gca tgg aaa	1536
Gln Met Thr Tyr Gly Ile Ser Ser Glu Lys Met Leu Lys Ala Trp Lys	
500 505 510	
gaa atg gaa gaa aag gcc atc cac tat gct gag gtt ggt gtc att gga	1584
Glu Met Glu Glu Lys Ala Ile His Tyr Ala Glu Val Gly Val Ile Gly	
515 520 525	
tac ctg gag gat cag att atg tct ttg cat gct gaa atc atg ggg cta	1632
Tyr Leu Glu Asp Gln Ile Met Ser Leu His Ala Glu Ile Met Gly Leu	
530 535 540	
cag aag agc ccc tat gga aga cgt cag gga gac ttg atg gaa tct ctg	1680
Gln Lys Ser Pro Tyr Gly Arg Arg Gln Gly Asp Leu Met Glu Ser Leu	
545 550 555 560	
gaa cag cgt gcc att gat cta tat aag cag tta aaa cac aga cct tca	1728
Glu Gln Arg Ala Ile Asp Leu Tyr Lys Gln Leu Lys His Arg Pro Ser	
565 570 575	
gat cac tcc tac agt gac agc aca gag atg gtg aaa atc att gtg cac	1776
Asp His Ser Tyr Ser Asp Ser Thr Glu Met Val Lys Ile Ile Val His	
580 585 590	
act gtg cag agt cag gac cgt gtg ctc aag gag ctg ttt ggt cat ttg	1824
Thr Val Gln Ser Gln Asp Arg Val Leu Lys Glu Leu Phe Gly His Leu	
595 600 605	
agc aag ttg ttg ggc tgt aag cag aag att att gat cta ctc cct aag	1872
Ser Lys Leu Leu Gly Cys Lys Gln Lys Ile Ile Asp Leu Leu Pro Lys	
610 615 620	
gtg gaa gtg gcc ctc agt aat atc aaa gaa gct gac aat act gtc atg	1920
Val Glu Val Ala Leu Ser Asn Ile Lys Glu Ala Asp Asn Thr Val Met	
625 630 635 640	
ttc atg cag gga aaa agg cag aaa gaa ata tgg cat ctc ctt aaa att	1968
Phe Met Gln Gly Lys Arg Gln Lys Glu Ile Trp His Leu Leu Lys Ile	
645 650 655	



gcc tgt aca cag agt tct gcc cgc tct ctt gta gga tcc agt cta gaa	2016
Ala Cys Thr Gln Ser Ser Ala Arg Ser Leu Val Gly Ser Ser Leu Glu	
660 665 670	
ggg gca gta acc cct cag aca tca gca tgg ctg ccc ccg act tca gca	2064
Gly Ala Val Thr Pro Gln Thr Ser Ala Trp Leu Pro Pro Thr Ser Ala	
675 680 685	
gaa cat gat cat tct ctg tca tgt gtg gta act cct caa gat ggg gag	2112
Glu His Asp His Ser Leu Ser Cys Val Val Thr Pro Gln Asp Gly Glu	
690 695 700	
act tca gca caa atg ata gaa gaa aat ttg aac tgc ctt ggc cat tta	2160
Thr Ser Ala Gln Met Ile Glu Glu Asn Leu Asn Cys Leu Gly His Leu	
705 710 715 720	
agc act att att cat gag gca aat gag gaa cag ggc aat agt atg atg	2208
Ser Thr Ile Ile His Glu Ala Asn Glu Glu Gln Gly Asn Ser Met Met	
725 730 735	
aat ctt gat tgg agt tgg tta aca gaa tgg gta ccg cgg gcc cgg gat	2256
Asn Leu Asp Trp Ser Trp Leu Thr Glu Trp Val Pro Arg Ala Arg Asp	
740 745 750	
cca ccg gtc gcc acc atg gtg agc aag ggc gag gag ctg ttc acc ggg	2304
Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly	
755 760 765	
gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag	2352
Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys	
770 775 780	
ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg	2400
Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu	
785 790 795 800	
acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc	2448
Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro	
805 810 815	
acc ctc gtg acc acc ctg acc tac ggc gtg cag tgc ttc agc cgc tac	2496
Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr	
820 825 830	
ccc gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa	2544
Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu	
835 840 845	
ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac	2592
Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr	
850 855 860	
aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc	2640
Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg	
865 870 875 880	
atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg	2688
Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly	
885 890 895	
cac aag ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc	2736
His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala	
900 905 910	
gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac	2784
Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn	
915 920 925	
atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc	2832
Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr	
930 935 940	
ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc	2880
Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser	
945 950 955 960	
acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg	2928
Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met	
965 970 975	
gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac	2976
Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp	
980 985 990	

gag ctg tac aag taa  
 Glu Leu Tyr Lys  
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2991

<210> 123

<211> 996

<212> PRT

<213> Artificial Sequence

<220>

<223> IkappaB-kinase-EGFP fusion

<400> 123

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Met	Arg	Glu	Arg	Leu	Gly	Thr	Gly	Gly	Phe	Gly	Asn	Val	Cys	Leu	Tyr	
			20					25					30			
Gln	His	Arg	Glu	Leu	Asp	Leu	Lys	Ile	Ala	Ile	Lys	Ser	Cys	Arg	Leu	
		35					40					45				
Glu	Leu	Ser	Thr	Lys	Asn	Arg	Glu	Arg	Trp	Cys	His	Glu	Ile	Gln	Ile	
	50				55						60					
Met	Lys	Lys	Leu	Asn	His	Ala	Asn	Val	Val	Lys	Ala	Cys	Asp	Val	Pro	
65				70					75						80	
Glu	Glu	Leu	Asn	Ile	Leu	Ile	His	Asp	Val	Pro	Leu	Leu	Ala	Met	Glu	
			85						90					95		
Tyr	Cys	Ser	Gly	Gly	Asp	Leu	Arg	Lys	Leu	Leu	Asn	Lys	Pro	Glu	Asn	
			100					105					110			
Cys	Cys	Gly	Leu	Lys	Glu	Ser	Gln	Ile	Leu	Ser	Leu	Leu	Ser	Asp	Ile	
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Gly	Ser	Gly	Ile	Arg	Tyr	Leu	His	Glu	Asn	Lys	Ile	Ile	His	Arg	Asp	
	130					135					140					
Leu	Lys	Pro	Glu	Asn	Ile	Val	Leu	Gln	Asp	Val	Gly	Gly	Lys	Ile	Ile	
145				150					155						160	
His	Lys	Ile	Ile	Asp	Leu	Gly	Tyr	Ala	Lys	Asp	Val	Asp	Gln	Gly	Ser	
			165					170						175		
Leu	Cys	Thr	Ser	Phe	Val	Gly	Thr	Leu	Gln	Tyr	Leu	Ala	Pro	Glu	Leu	
		180						185					190			
Phe	Glu	Asn	Lys	Pro	Tyr	Thr	Ala	Thr	Val	Asp	Tyr	Trp	Ser	Phe	Gly	
	195					200						205				
Thr	Met	Val	Phe	Glu	Cys	Ile	Ala	Gly	Tyr	Arg	Pro	Phe	Leu	His	His	
	210				215						220					
Leu	Gln	Pro	Phe	Thr	Trp	His	Glu	Lys	Ile	Lys	Lys	Lys	Asp	Pro	Lys	
225				230					235						240	
Cys	Ile	Phe	Ala	Cys	Glu	Glu	Met	Ser	Gly	Glu	Val	Arg	Phe	Ser	Ser	
			245						250					255		
His	Leu	Pro	Gln	Pro	Asn	Ser	Leu	Cys	Ser	Leu	Ile	Val	Glu	Pro	Met	
		260					265						270			
Glu	Asn	Trp	Leu	Gln	Leu	Met	Leu	Asn	Trp	Asp	Pro	Gln	Gln	Arg	Gly	
	275					280						285				
Gly	Pro	Val	Asp	Leu	Thr	Leu	Lys	Gln	Pro	Arg	Cys	Phe	Val	Leu	Met	
	290				295						300					
Asp	His	Ile	Leu	Asn	Leu	Lys	Ile	Val	His	Ile	Leu	Asn	Met	Thr	Ser	
305				310					315						320	
Ala	Lys	Ile	Ile	Ser	Phe	Leu	Leu	Pro	Pro	Asp	Glu	Ser	Leu	His	Ser	
			325						330					335		
Leu	Gln	Ser	Arg	Ile	Glu	Arg	Glu	Thr	Gly	Ile	Asn	Thr	Gly	Ser	Gln	

														340						345						350		
Glu	Leu	Leu	Ser	Glu	Thr	Gly	Ile	Ser	Leu	Asp	Pro	Arg	Lys	Pro	Ala													
		355					360					365																
Ser	Gln	Cys	Val	Leu	Asp	Gly	Val	Arg	Gly	Cys	Asp	Ser	Tyr	Met	Val													
		370				375				380																		
Tyr	Leu	Phe	Asp	Lys	Ser	Lys	Thr	Val	Tyr	Glu	Gly	Pro	Phe	Ala	Ser													
385					390				395																			
Arg	Ser	Leu	Ser	Asp	Cys	Val	Asn	Tyr	Ile	Val	Gln	Asp	Ser	Lys	Ile													
		405				410				415																		
Gln	Leu	Pro	Ile	Ile	Gln	Leu	Arg	Lys	Val	Trp	Ala	Glu	Ala	Val	His													
		420				425				430																		
Tyr	Val	Ser	Gly	Leu	Lys	Glu	Asp	Tyr	Ser	Arg	Leu	Phe	Gln	Gly	Gln													
		435				440				445																		
Arg	Ala	Ala	Met	Leu	Ser	Leu	Leu	Arg	Tyr	Asn	Ala	Asn	Leu	Thr	Lys													
		450				455				460																		
Met	Lys	Asn	Thr	Leu	Ile	Ser	Ala	Ser	Gln	Gln	Leu	Lys	Ala	Lys	Leu													
465					470				475																			
Glu	Phe	Phe	His	Lys	Ser	Ile	Gln	Leu	Asp	Leu	Glu	Arg	Tyr	Ser	Glu													
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Gln	Met	Thr	Tyr	Gly	Ile	Ser	Ser	Glu	Lys	Met	Leu	Lys	Ala	Trp	Lys													
		500				505				510																		
Glu	Met	Glu	Glu	Lys	Ala	Ile	His	Tyr	Ala	Glu	Val	Gly	Val	Ile	Gly													
		515				520				525																		
Tyr	Leu	Glu	Asp	Gln	Ile	Met	Ser	Leu	His	Ala	Glu	Ile	Met	Gly	Leu													
		530				535				540																		
Gln	Lys	Ser	Pro	Tyr	Gly	Arg	Arg	Gln	Gly	Asp	Leu	Met	Glu	Ser	Leu													
545					550				555																			
Glu	Gln	Arg	Ala	Ile	Asp	Leu	Tyr	Lys	Gln	Leu	Lys	His	Arg	Pro	Ser													
		565				570				575																		
Asp	His	Ser	Tyr	Ser	Asp	Ser	Thr	Glu	Met	Val	Lys	Ile	Ile	Val	His													
		580				585				590																		
Thr	Val	Gln	Ser	Gln	Asp	Arg	Val	Leu	Lys	Glu	Leu	Phe	Gly	His	Leu													
		595				600				605																		
Ser	Lys	Leu	Leu	Gly	Cys	Lys	Gln	Lys	Ile	Ile	Asp	Leu	Leu	Pro	Lys													
		610				615				620																		
Val	Glu	Val	Ala	Leu	Ser	Asn	Ile	Lys	Glu	Ala	Asp	Asn	Thr	Val	Met													
625					630				635																			
Phe	Met	Gln	Gly	Lys	Arg	Gln	Lys	Glu	Ile	Trp	His	Leu	Leu	Lys	Ile													
		645				650				655																		
Ala	Cys	Thr	Gln	Ser	Ser	Ala	Arg	Ser	Leu	Val	Gly	Ser	Ser	Leu	Glu													
		660				665				670																		
Gly	Ala	Val	Thr	Pro	Gln	Thr	Ser	Ala	Trp	Leu	Pro	Pro	Thr	Ser	Ala													
		675				680				685																		
Glu	His	Asp	His	Ser	Leu	Ser	Cys	Val	Val	Thr	Pro	Gln	Asp	Gly	Glu													
		690																										

Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr  
 850 855 860  
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg  
 865 870 875 880  
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly  
 885 890 895  
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala  
 900 905 910  
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn  
 915 920 925  
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr  
 930 935 940  
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser  
 945 950 955 960  
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met  
 965 970 975  
 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp  
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 Glu Leu Tyr Lys  
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<210> 124

<211> 1908

<212> DNA

<213> Artificial Sequence

<220>

<223> EGFP-VASP fusion

<220>

<221> CDS

<222> (1)..(1905)

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc		96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly		
20 25 30		
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc		144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile		
35 40 45		
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc		192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr		
50 55 60		
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag		240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys		
65 70 75 80		
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag		288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		
85 90 95		

cg	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cg	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105						110		
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cg	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120						125			
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
		130				135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
					150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cg	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
			165					170						175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
			180					185						190		
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
			195			200						205				
agc	aaa	gac	ccc	aac	gag	aag	cg	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
		210				215					220					
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc	720
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
		225			230					235					240	
gga	ctc	aga	tct	cga	gct	caa	gct	tcc	atg	agc	gag	acg	gtc	atc	atg	768
Gly	Leu	Arg	Ser	Arg	Ala	Gln	Ala	Ser	Met	Ser	Glu	Thr	Val	Ile	Met	
				245				250						255		
agc	gag	acg	gtc	atc	tgt	tcc	agc	cg	gcc	act	gtg	atg	ctt	tat	gat	816
Ser	Glu	Thr	Val	Ile	Cys	Ser	Ser	Arg	Ala	Thr	Val	Met	Leu	Tyr	Asp	
			260				265						270			
gat	ggc	aac	aag	cga	tgg	ctc	cct	gct	ggc	acg	ggt	ccc	cag	gcc	ttc	864
Asp	Gly	Asn	Lys	Arg	Trp	Leu	Pro	Ala	Gly	Thr	Gly	Pro	Gln	Ala	Phe	
		275				280						285				
agc	cg	gtc	cag	atc	tac	cac	aac	ccc	acg	gcc	aat	tcc	ttt	cg	gtc	912
Ser	Arg	Val	Gln	Ile	Tyr	His	Asn	Pro	Thr	Ala	Asn	Ser	Phe	Arg	Val	
		290				295					300					
gtg	ggc	cg	aag	atg	cag	ccc	gac	cag	cag	gtg	gtc	atc	aac	tgt	gcc	960
Val	Gly	Arg	Lys	Met	Gln	Pro	Asp	Gln	Gln	Val	Val	Ile	Asn	Cys	Ala	
		305			310					315					320	
atc	gtc	cg	ggt	gtc	aag	tat	aac	cag	gcc	acc	ccc	aac	ttc	cat	cag	1008
Ile	Val	Arg	Gly	Val	Lys	Tyr	Asn	Gln	Ala	Thr	Pro	Asn	Phe	His	Gln	
				325				330					335			
tgg	cg	gac	gct	cg	cag	gtc	tgg	ggc	ctc	aac	ttc	ggc	agc	aag	gag	1056
Trp	Arg	Asp	Ala	Arg	Gln	Val	Trp	Gly	Leu	Asn	Phe	Gly	Ser	Lys	Glu	
			340					345					350			
gat	gcg	gcc	cag	ttt	gcc	gcc	ggc	atg	gcc	agt	gcc	cta	gag	gcg	ttg	1104
Asp	Ala	Ala	Gln	Phe	Ala	Ala	Gly	Met	Ala	Ser	Ala	Leu	Glu	Ala	Leu	
		355					360					365				
gaa	gga	ggt	ggg	ccc	cct	cca	ccc	cca	gca	ctt	ccc	acc	tgg	tcg	gtc	1152
Glu	Gly	Gly	Gly	Pro	Pro	Pro	Pro	Pro	Ala	Leu	Pro	Thr	Trp	Ser	Val	
		370				375					380					
ccg	aac	ggc	ccc	tcc	ccg	gag	gag	gtg	gag	cag	cag	aaa	agg	cag	cag	1200
Pro	Asn	Gly	Pro	Ser	Pro	Glu	Glu	Val	Glu	Gln	Lys	Arg	Gln	Gln		
					390					395					400	
ccc	ggc	ccg	tcg	gag	cac	ata	gag	cg	cg	gtc	tcc	aat	gca	gga	ggc	1248
Pro	Gly	Pro	Ser	Glu	His	Ile	Glu	Arg	Arg	Val	Ser	Asn	Ala	Gly	Gly	
				405				410						415		
cca	cct	gct	ccc	ccc	gct	ggg	ggt	cca	ccc	cca	cca	cca	gga	cct	ccc	1296
Pro	Pro	Ala	Pro	Pro	Ala	Gly	Gly	Pro	Pro	Pro	Pro	Pro	Gly	Pro	Pro	
			420					425					430			

cct cct cca ggt ccc ccc cca ccc cca ggt ttg ccc cct tcg ggg gtc	1344
Pro Pro Pro Gly Pro Pro Pro Pro Gly Leu Pro Pro Ser Gly Val	
435 440 445	
cca gct gca gcg cac gga gca ggg gga gga cca ccc cct gca ccc cct	1392
Pro Ala Ala Ala His Gly Ala Gly Gly Gly Pro Pro Pro Ala Pro Pro	
450 455 460	
ctc ccg gca gca cag ggc cct ggt ggt ggg gga gct ggg gcc cca ggc	1440
Leu Pro Ala Ala Gln Gly Pro Gly Gly Gly Ala Gly Ala Pro Gly	
465 470 475 480	
ctg gcc gca gct att gct gga gcc aaa ctc agg aaa gtc agc aag cag	1488
Leu Ala Ala Ala Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Lys Gln	
485 490 495	
gag gag gcc tca ggg ggg ccc aca gcc ccc aaa gct gag agt ggt cga	1536
Glu Glu Ala Ser Gly Gly Pro Thr Ala Pro Lys Ala Glu Ser Gly Arg	
500 505 510	
agc gga ggt ggg gga ctc atg gaa gag atg aac gcc atg ctg gcc cgg	1584
Ser Gly Gly Gly Gly Leu Met Glu Glu Met Asn Ala Met Leu Ala Arg	
515 520 525	
aga agg aaa gcc acg caa gtt ggg gag aaa acc ccc aag gat gaa tct	1632
Arg Arg Lys Ala Thr Gln Val Gly Glu Lys Thr Pro Lys Asp Glu Ser	
530 535 540	
gcc aat cag gag gag cca gag gcc aga gtc ccg gcc cag agt gaa tct	1680
Ala Asn Gln Glu Glu Pro Glu Ala Arg Val Pro Ala Gln Ser Glu Ser	
545 550 555 560	
gtg cgg aga ccc tgg gag aag aac agc aca acc ttg cca agg atg aag	1728
Val Arg Arg Pro Trp Glu Lys Asn Ser Thr Thr Leu Pro Arg Met Lys	
565 570 575	
tcg tct tct tcg gtg acc act tcc gag acc caa ccc tgc acg ccc agc	1776
Ser Ser Ser Ser Val Thr Thr Ser Glu Thr Gln Pro Cys Thr Pro Ser	
580 585 590	
tcc agt gat tac tcg gac cta cag agg gtg aaa cag gag ctt ctg gaa	1824
Ser Ser Asp Tyr Ser Asp Leu Gln Arg Val Lys Gln Glu Leu Leu Glu	
595 600 605	
gag gtg aag aag gaa ttg cag aaa gtg aaa gag gaa atc att gaa gcc	1872
Glu Val Lys Lys Glu Leu Gln Lys Val Lys Glu Glu Ile Ile Glu Ala	
610 615 620	
ttc gtc cag gag ctg agg aag cgg ggt tct ccc tga	1908
Phe Val Gln Glu Leu Arg Lys Arg Gly Ser Pro	
625 630 635	

<210> 125

<211> 635

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-VASP fusion

<400> 125

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1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	

50	55	60
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys		
65	70	75
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu		80
	85	90
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu		95
	100	105
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		110
	115	120
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		125
	130	135
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		140
145	150	155
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		160
	165	170
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		175
	180	185
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		190
	195	200
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		205
210	215	220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		225
	230	235
Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ser Glu Thr Val Ile Met		240
	245	250
Ser Glu Thr Val Ile Cys Ser Ser Arg Ala Thr Val Met Leu Tyr Asp		255
	260	265
Asp Gly Asn Lys Arg Trp Leu Pro Ala Gly Thr Gly Pro Gln Ala Phe		270
	275	280
Ser Arg Val Gln Ile Tyr His Asn Pro Thr Ala Asn Ser Phe Arg Val		285
	290	295
Val Gly Arg Lys Met Gln Pro Asp Gln Gln Val Val Ile Asn Cys Ala		300
305	310	315
Ile Val Arg Gly Val Lys Tyr Asn Gln Ala Thr Pro Asn Phe His Gln		320
	325	330
Trp Arg Asp Ala Arg Gln Val Trp Gly Leu Asn Phe Gly Ser Lys Glu		335
	340	345
Asp Ala Ala Gln Phe Ala Ala Gly Met Ala Ser Ala Leu Glu Ala Leu		350
	355	360
Glu Gly Gly Gly Pro Pro Pro Pro Pro Ala Leu Pro Thr Trp Ser Val		365
	370	375
Pro Asn Gly Pro Ser Pro Glu Glu Val Glu Gln Gln Lys Arg Gln Gln		380
385	390	395
Pro Gly Pro Ser Glu His Ile Glu Arg Arg Val Ser Asn Ala Gly Gly		400
	405	410
Pro Pro Ala Pro Pro Ala Gly Gly Pro Pro Pro Pro Pro Gly Pro Pro		415
	420	425
Pro Pro Pro Gly Pro Pro Pro Pro Gly Leu Pro Pro Ser Gly Val		430
	435	440
Pro Ala Ala Ala His Gly Ala Gly Gly Gly Pro Pro Ala Pro Pro		445
	450	455
Leu Pro Ala Ala Gln Gly Pro Gly Gly Gly Gly Ala Gly Ala Pro Gly		460
465	470	475
Leu Ala Ala Ala Ile Ala Gly Ala Lys Leu Arg Lys Val Ser Lys Gln		480
	485	490
Glu Glu Ala Ser Gly Gly Pro Thr Ala Pro Lys Ala Glu Ser Gly Arg		495
	500	505
Ser Gly Gly Gly Gly Leu Met Glu Glu Met Asn Ala Met Leu Ala Arg		510
	515	520
Arg Arg Lys Ala Thr Gln Val Gly Glu Lys Thr Pro Lys Asp Glu Ser		525
	530	535
Ala Asn Gln Glu Glu Pro Glu Ala Arg Val Pro Ala Gln Ser Glu Ser		540
545	550	555
		560





Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctg ggc atg gac gag ctg tac aag tcc	720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
225 230 235 240	
gga ctg aga tct cga gct caa gct tca atg gct gcc atc cgg aag aaa	768
Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ala Ala Ile Arg Lys Lys	
245 250 255	
ctg gtg att gtt ggt gat gga gcc tgt gga aag aca tgc ttg ctg ata	816
Leu Val Ile Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile	
260 265 270	
gtc ttc agc aag gac cag ttc cca gag gtg tat gtg ccc aca gtg ttt	864
Val Phe Ser Lys Asp Gln Phe Pro Glu Val Tyr Val Thr Val Phe	
275 280 285	
gag aac tat gtg gca gat atc gag gtg gat gga aag cag gta gag ttg	912
Glu Asn Tyr Val Ala Asp Ile Glu Val Asp Gly Lys Gln Val Glu Leu	
290 295 300	
gct ttg tgg gac aca gct ggg cag gaa gat tat gat cgc ctg agg ccc	960
Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro	
305 310 315 320	
ctc tcc tac cca gat acc gat gtt ata ctg atg tgt ttt tcc atc gac	1008
Leu Ser Tyr Pro Asp Thr Asp Val Ile Leu Met Cys Phe Ser Ile Asp	
325 330 335	
agc cct gat agt tta gaa aac atc cca gaa aag tgg acc cca gaa gtc	1056
Ser Pro Asp Ser Leu Glu Asn Ile Pro Glu Lys Trp Thr Pro Glu Val	
340 345 350	
aag cat ttc tgt ccc aac gtg ccc atc atc ctg gtt ggg aat aag aag	1104
Lys His Phe Cys Pro Asn Val Pro Ile Ile Leu Val Gly Asn Lys Lys	
355 360 365	
gat ctt cgg aat gat gag cac aca agg cgg gag cta gcc aag atg aag	1152
Asp Leu Arg Asn Asp Glu His Thr Arg Arg Glu Leu Ala Lys Met Lys	
370 375 380	
cag gag ccg gtg aaa cct gaa gaa ggc aga gat atg gca aac agg att	1200
Gln Glu Pro Val Lys Pro Glu Glu Gly Arg Asp Met Ala Asn Arg Ile	
385 390 395 400	
ggc gct ttt ggg tac atg gag tgt tca gca aag acc aaa gat gga gtg	1248
Gly Ala Phe Gly Tyr Met Glu Cys Ser Ala Lys Thr Lys Asp Gly Val	
405 410 415	
aga gag gtt ttt gaa atg gct acg aga gct gct ctg caa gct aga cgt	1296
Arg Glu Val Phe Glu Met Ala Thr Arg Ala Ala Leu Gln Ala Arg Arg	
420 425 430	
ggg aag aaa aaa tct ggt tgc ctt gtc ttg tga	1329
Gly Lys Lys Lys Ser Gly Cys Leu Val Leu	
435 440	

<210> 127

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-RhoA fusion

<400> 127

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20     25     30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35     40     45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50     55     60
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65     70     75     80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85     90     95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100    105    110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115    120    125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130    135    140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145    150    155    160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165    170    175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180    185    190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195    200    205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210    215    220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225    230    235    240
Gly Leu Arg Ser Arg Ala Gln Ala Ser Met Ala Ala Ile Arg Lys Lys
245    250    255
Leu Val Ile Val Gly Asp Gly Ala Cys Gly Lys Thr Cys Leu Leu Ile
260    265    270
Val Phe Ser Lys Asp Gln Phe Pro Glu Val Tyr Val Pro Thr Val Phe
275    280    285
Glu Asn Tyr Val Ala Asp Ile Glu Val Asp Gly Lys Gln Val Glu Leu
290    295    300
Ala Leu Trp Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro
305    310    315    320
Leu Ser Tyr Pro Asp Thr Asp Val Ile Leu Met Cys Phe Ser Ile Asp
325    330    335
Ser Pro Asp Ser Leu Glu Asn Ile Pro Glu Lys Trp Thr Pro Glu Val
340    345    350
Lys His Phe Cys Pro Asn Val Pro Ile Ile Leu Val Gly Asn Lys Lys
355    360    365
Asp Leu Arg Asn Asp Glu His Thr Arg Arg Glu Leu Ala Lys Met Lys
370    375    380
Gln Glu Pro Val Lys Pro Glu Glu Gly Arg Asp Met Ala Asn Arg Ile
385    390    395    400
Gly Ala Phe Gly Tyr Met Glu Cys Ser Ala Lys Thr Lys Asp Gly Val
405    410    415
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Arg Glu Val Phe Glu Met Ala Thr Arg Ala Ala Leu Gln Ala Arg Arg  
420 425 430  
Gly Lys Lys Lys Ser Gly Cys Leu Val Leu  
435 440

<210> 128

<211> 1140

<212> DNA

<213> Artificial Sequence

<220>

<223> actin-binding-domain-EGFP fusion

<220>

<221> CDS

<222> (1)..(1137)

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Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu  
1 5 10 15  
gag gac tgg gac cgg gac ctg ctc ctg gac ccg gcc tgg gag aag cag 96  
Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln  
20 25 30  
cag aga aag aca ttc acg gca tgg tgt aac tcc cac ctc cgg aag gcg 144  
Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala  
35 40 45  
ggg aca cag atc gag aac atc gaa gag gac ttc cgg gat ggc ctg aag 192  
Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys  
50 55 60  
ctc atg ctg ctg ctg gag gtc atc tca ggt gaa cgc ttg gcc aag cca 240  
Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro  
65 70 75 80  
gag cga ggc aag atg aga gtg cac aag atc tcc aac gtc aac aag gcc 288  
Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala  
85 90 95  
ctg gat ttc ata gcc agc aaa ggc gtc aaa ctg gtg tcc atc gga gcc 336  
Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala  
100 105 110  
gaa gaa atc gtg gat ggg aat gtg aag atg acc ctg ggc atg atc tgg 384  
Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp  
115 120 125  
acc atc atc ctg cgc agg gat cca ccg gtc gcc acc atg gtg agc aag 432  
Thr Ile Ile Leu Arg Arg Asp Pro Pro Val Ala Thr Met Val Ser Lys  
130 135 140  
ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac 480  
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp  
145 150 155 160  
ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc 528  
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly  
165 170 175  
gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc 576

Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly		
			180					185					190				
aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg	acc	tac	ggc	624	
Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly		
		195					200					205					
gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	cag	cac	gac	ttc	672	
Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe		
	210					215					220						
ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	acc	atc	ttc	720	
Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe		
225					230					235					240		
ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	aag	ttc	gag	768	
Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu		
				245					250					255			
ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	gac	ttc	aag	816	
Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys		
			260					265					270				
gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	tac	aac	agc	864	
Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser		
		275					280					285					
cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	atc	aag	gtg	912	
His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val		
	290					295						300					
aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	960	
Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala		
305					310					315					320		
gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	1008	
Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu		
				325					330					335			
ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	1056	
Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro		
			340					345					350				
aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	1104	
Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala		
		355					360					365					
ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	taa					1140	
Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys							
	370					375											

<210> 129

<211> 379

<212> PRT

<213> Artificial Sequence

<220>

<223> actin-binding-domain-EGFP fusion

<400> 129

Met	Asp	His	Tyr	Asp	Ser	Gln	Gln	Thr	Asn	Asp	Tyr	Met	Gln	Pro	Glu		
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Glu	Asp	Trp	Asp	Arg	Asp	Leu	Leu	Leu	Asp	Pro	Ala	Trp	Glu	Lys	Gln		
			20					25					30				
Gln	Arg	Lys	Thr	Phe	Thr	Ala	Trp	Cys	Asn	Ser	His	Leu	Arg	Lys	Ala		
		35				40					45						
Gly	Thr	Gln	Ile	Glu	Asn	Ile	Glu	Glu	Asp	Phe	Arg	Asp	Gly	Leu	Lys		
	50					55					60						

Leu	Met	Leu	Leu	Leu	Glu	Val	Ile	Ser	Gly	Glu	Arg	Leu	Ala	Lys	Pro
65					70					75					80
Glu	Arg	Gly	Lys	Met	Arg	Val	His	Lys	Ile	Ser	Asn	Val	Asn	Lys	Ala
				85					90					95	
Leu	Asp	Phe	Ile	Ala	Ser	Lys	Gly	Val	Lys	Leu	Val	Ser	Ile	Gly	Ala
			100					105					110		
Glu	Glu	Ile	Val	Asp	Gly	Asn	Val	Lys	Met	Thr	Leu	Gly	Met	Ile	Trp
		115					120					125			
Thr	Ile	Ile	Leu	Arg	Arg	Asp	Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys
	130					135						140			
Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp
145					150					155					160
Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly
			165					170						175	
Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly
			180					185					190		
Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly
		195				200						205			
Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe
	210					215					220				
Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe
225					230					235					240
Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu
			245					250						255	
Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys
			260					265					270		
Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser
		275					280					285			
His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val
	290					295					300				
Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala
305					310					315					320
Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu
			325						330					335	
Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro
			340					345					350		
Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala
		355					360					365			
Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys					
	370					375									

<210> 130

<211> 3516

<212> DNA

<213> Artificial Sequence

<220>

<223> EGFP-NFAT fusion

<220>

<221> CDS

<222> (1)..(3513)



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Leu Ala Ser Leu Ser Gly Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp	
325 330 335	
agg gta ggg ccg cag aag ttt ctg agc gcg gcc aag cca gca ggg gcc	1056
Arg Val Gly Pro Gln Lys Phe Leu Ser Ala Ala Lys Pro Ala Gly Ala	
340 345 350	
tcg ggc ctg agc cct cgg atc gag atc act ccg tcc cac gaa ctg atc	1104
Ser Gly Leu Ser Pro Arg Ile Glu Ile Thr Pro Ser His Glu Leu Ile	
355 360 365	
cag gca gtg ggg ccc ctc cgc atg aga gac gcg ggc ctc ctg gtg gag	1152
Gln Ala Val Gly Pro Leu Arg Met Arg Asp Ala Gly Leu Leu Val Glu	
370 375 380	
cag cct ccc ctg gcc ggg gtg gcc gcc agc ccg agg ttc acc ctg ccc	1200
Gln Pro Pro Leu Ala Gly Val Ala Ala Ser Pro Arg Phe Thr Leu Pro	
385 390 395 400	
gtg ccc ggc ttc gag ggc tac cgc gag ccg ctt tgc ttg agc ccc gct	1248
Val Pro Gly Phe Glu Gly Tyr Arg Glu Pro Leu Cys Leu Ser Pro Ala	
405 410 415	
agc agc ggc tcc tct gcc agc ttc att tct gac acc ttc tcc ccc tac	1296
Ser Ser Gly Ser Ser Ala Ser Phe Ile Ser Asp Thr Phe Ser Pro Tyr	
420 425 430	
acc tcg ccc tgc gtc tcg ccc aat aac ggc ggg ccc gac gac ctg tgt	1344
Thr Ser Pro Cys Val Ser Pro Asn Asn Gly Gly Pro Asp Asp Leu Cys	
435 440 445	
ccg cag ttt caa aac atc cct gct cat tat tcc ccc aga acc tcg cca	1392
Pro Gln Phe Gln Asn Ile Pro Ala His Tyr Ser Pro Arg Thr Ser Pro	
450 455 460	
ata atg tca cct cga acc agc ctc gcc gag gac agc tgc ctg ggc cgc	1440
Ile Met Ser Pro Arg Thr Ser Leu Ala Glu Asp Ser Cys Leu Gly Arg	
465 470 475 480	
cac tcg ccc gtg ccc cgt ccg gcc tcc cgc tcc tca tcg cct ggt gcc	1488
His Ser Pro Val Pro Arg Pro Ala Ser Arg Ser Ser Ser Pro Gly Ala	
485 490 495	
aag cgg agg cat tcg tgc gcc gag gcc ttg gtt gcc ctg ccg ccc gga	1536
Lys Arg Arg His Ser Cys Ala Glu Ala Leu Val Ala Leu Pro Pro Gly	
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Ala Ser Pro Gln Arg Ser Arg Ser Pro Ser Pro Gln Pro Ser Ser His	
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Val Ala Pro Gln Asp His Gly Ser Pro Ala Gly Tyr Pro Pro Val Ala	
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ggc tct gcc gtg atc atg gat gcc ctg aac agc ctc gcc acg gac tcg	1680
Gly Ser Ala Val Ile Met Asp Ala Leu Asn Ser Leu Ala Thr Asp Ser	
545 550 555 560	
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Pro Cys Gly Ile Pro Pro Lys Met Trp Lys Thr Ser Pro Asp Pro Ser	
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Pro Val Ser Ala Ala Pro Ser Lys Ala Gly Leu Pro Arg His Ile Tyr	
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Pro Ala Val Glu Phe Leu Gly Pro Cys Glu Gln Gly Glu Arg Arg Asn	
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Ser Ala Pro Glu Ser Ile Leu Leu Val Pro Pro Thr Trp Pro Lys Pro	
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Leu Val Pro Ala Ile Pro Ile Cys Ser Ile Pro Val Thr Ala Ser Leu	
625 630 635 640	
cct cca ctt gag tgg ccg ctg tcc agt cag tca ggc tct tac gag ctg	1968
Pro Pro Leu Glu Trp Pro Leu Ser Ser Gln Ser Gly Ser Tyr Glu Leu	
645 650 655	

cgg atc gag gtg cag ccc aag cca cat cac cgg gcc cac tat gag aca	2016
Arg Ile Glu Val Gln Pro Lys Pro His His Arg Ala His Tyr Glu Thr	
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Glu Gly Ser Arg Gly Ala Val Lys Ala Pro Thr Gly Gly His Pro Val	
675 680 685	
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Val Gln Leu His Gly Tyr Met Glu Asn Lys Pro Leu Gly Leu Gln Ile	
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Phe Ile Gly Thr Ala Asp Glu Arg Ile Leu Lys Pro His Ala Phe Tyr	
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Gln Val His Arg Ile Thr Gly Lys Thr Val Thr Thr Thr Ser Tyr Glu	
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Lys Ile Val Gly Asn Thr Lys Val Leu Glu Ile Pro Leu Glu Pro Lys	
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Asn Asn Met Arg Ala Thr Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg	
755 760 765	
aac gcc gac att gag ctg cgg aaa ggc gag acg gac att gga aga aag	2352
Asn Ala Asp Ile Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys	
770 775 780	
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Asn Thr Arg Val Arg Leu Val Phe Arg Val His Ile Pro Glu Ser Ser	
785 790 795 800	
ggc aga atc gtc tct tta cag act gca tct aac ccc atc gag tgc tcc	2448
Gly Arg Ile Val Ser Leu Gln Thr Ala Ser Asn Pro Ile Glu Cys Ser	
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Gln Arg Ser Ala His Glu Leu Pro Met Val Glu Arg Gln Asp Thr Asp	
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agc tgc ctg gtc tat ggc ggc cag caa atg atc ctc acg ggg cag aac	2544
Ser Cys Leu Val Tyr Gly Gly Gln Gln Met Ile Leu Thr Gly Gln Asn	
835 840 845	
ttt aca tcc gag tcc aaa gtt gtg ttt act gag aag acc aca gat gga	2592
Phe Thr Ser Glu Ser Lys Val Phe Thr Glu Lys Thr Thr Asp Gly	
850 855 860	
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Gln Gln Ile Trp Glu Met Glu Ala Thr Val Asp Lys Asp Lys Ser Gln	
865 870 875 880	
ccc aac atg ctt ttt gtt gag atc cct gaa tat cgg aac aag cat atc	2688
Pro Asn Met Leu Phe Val Glu Ile Pro Glu Tyr Arg Asn Lys His Ile	
885 890 895	
cgc aca cct gta aaa gtg aac ttc tac gtc atc aat ggg aag aga aaa	2736
Arg Thr Pro Val Lys Val Asn Phe Tyr Val Ile Asn Gly Lys Arg Lys	
900 905 910	
cga agt cag cct cag cac ttt acc tac cac cca gtc cca gcc atc aag	2784
Arg Ser Gln Pro Gln His Phe Thr Tyr His Pro Val Pro Ala Ile Lys	
915 920 925	
acg gag ccc acg gat gaa tat gac ccc act ctg atc tgc agc ccc acc	2832
Thr Glu Pro Thr Asp Glu Tyr Asp Pro Thr Leu Ile Cys Ser Pro Thr	
930 935 940	
cat gga ggc ctg ggg agc cag cct tac tac ccc cag cac ccg atg gtg	2880
His Gly Gly Leu Gly Ser Gln Pro Tyr Tyr Pro Gln His Pro Met Val	
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gcc gag tcc ccc tcc tgc ctc gtg gcc acc atg gct ccc tgc cag cag	2928
Ala Glu Ser Pro Ser Cys Leu Val Ala Thr Met Ala Pro Cys Gln Gln	
965 970 975	
ttc cgc acg ggg ctc tca tcc cct gac gcc cgc tac cag caa cag aac	2976
Phe Arg Thr Gly Leu Ser Ser Pro Asp Ala Arg Tyr Gln Gln Asn	
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cca gcg gcc gta ctc tac cag cgg agc aag agc ctg agc ccc agc ctg 3024
Pro Ala Ala Val Leu Tyr Gln Arg Ser Lys Ser Leu Ser Pro Ser Leu
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ctg ggc tat cag cag ccg gcc ctc atg gcc gcc ccg ctg tcc ctt 3069
Leu Gly Tyr Gln Gln Pro Ala Leu Met Ala Ala Pro Leu Ser Leu
          1010                1015                1020
gcg gac gct cac cgc tct gtg ctg gtg cac gcc ggc tcc cag ggc 3114
Ala Asp Ala His Arg Ser Val Leu Val His Ala Gly Ser Gln Gly
          1025                1030                1035
cag agc tca gcc ctg ctc cac ccc tct ccg acc aac cag cag gcc 3159
Gln Ser Ser Ala Leu Leu His Pro Ser Pro Thr Asn Gln Gln Ala
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tcg cct gtg atc cac tac tca ccc acc aac cag cag ctg cgc tgc 3204
Ser Pro Val Ile His Tyr Ser Pro Thr Asn Gln Gln Leu Arg Cys
          1055                1060                1065
gga agc cac cag gag ttc cag cac atc atg tac tgc gag aat ttc 3249
Gly Ser His Gln Glu Phe Gln His Ile Met Tyr Cys Glu Asn Phe
          1070                1075                1080
gca cca ggc acc acc aga cct ggc ccg ccc ccg gtc agt caa ggt 3294
Ala Pro Gly Thr Thr Arg Pro Gly Pro Pro Pro Val Ser Gln Gly
          1085                1090                1095
cag agg ctg agc ccg ggt tcc tac ccc aca gtc att cag cag cag 3339
Gln Arg Leu Ser Pro Gly Ser Tyr Pro Thr Val Ile Gln Gln Gln
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aat gcc acg agc caa aga gcc gcc aaa aac gga ccc ccg gtc agt 3384
Asn Ala Thr Ser Gln Arg Ala Ala Lys Asn Gly Pro Pro Val Ser
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Asp Gln Lys Glu Val Leu Pro Ala Gly Val Thr Ile Lys Gln Glu
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cag aac ttg gac cag acc tac ttg gat gat gtt aat gaa att atc 3474
Gln Asn Leu Asp Gln Thr Tyr Leu Asp Asp Val Asn Glu Ile Ile
          1145                1150                1155
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<211> 1171

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-NFAT fusion

<400> 131

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
          35          40          45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
          50          55          60
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65          70          75          80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

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Pro Ala Val Glu Phe Leu Gly Pro Cys Glu Gln Gly Glu Arg Arg Asn  
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 Ser Ala Pro Glu Ser Ile Leu Leu Val Pro Pro Thr Trp Pro Lys Pro  
 610 615 620  
 Leu Val Pro Ala Ile Pro Ile Cys Ser Ile Pro Val Thr Ala Ser Leu  
 625 630 635 640  
 Pro Pro Leu Glu Trp Pro Leu Ser Ser Gln Ser Gly Ser Tyr Glu Leu  
 645 650 655  
 Arg Ile Glu Val Gln Pro Lys Pro His His Arg Ala His Tyr Glu Thr  
 660 665 670  
 Glu Gly Ser Arg Gly Ala Val Lys Ala Pro Thr Gly Gly His Pro Val  
 675 680 685  
 Val Gln Leu His Gly Tyr Met Glu Asn Lys Pro Leu Gly Leu Gln Ile  
 690 695 700  
 Phe Ile Gly Thr Ala Asp Glu Arg Ile Leu Lys Pro His Ala Phe Tyr  
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 Gln Val His Arg Ile Thr Gly Lys Thr Val Thr Thr Thr Ser Tyr Glu  
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 Lys Ile Val Gly Asn Thr Lys Val Leu Glu Ile Pro Leu Glu Pro Lys  
 740 745 750  
 Asn Asn Met Arg Ala Thr Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg  
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 Asn Ala Asp Ile Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys  
 770 775 780  
 Asn Thr Arg Val Arg Leu Val Phe Arg Val His Ile Pro Glu Ser Ser  
 785 790 795 800  
 Gly Arg Ile Val Ser Leu Gln Thr Ala Ser Asn Pro Ile Glu Cys Ser  
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 Gln Arg Ser Ala His Glu Leu Pro Met Val Glu Arg Gln Asp Thr Asp  
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 Ser Cys Leu Val Tyr Gly Gly Gln Gln Met Ile Leu Thr Gly Gln Asn  
 835 840 845  
 Phe Thr Ser Glu Ser Lys Val Phe Thr Glu Lys Thr Thr Asp Gly  
 850 855 860  
 Gln Gln Ile Trp Glu Met Glu Ala Thr Val Asp Lys Asp Lys Ser Gln  
 865 870 875 880  
 Pro Asn Met Leu Phe Val Glu Ile Pro Glu Tyr Arg Asn Lys His Ile  
 885 890 895  
 Arg Thr Pro Val Lys Val Asn Phe Tyr Val Ile Asn Gly Lys Arg Lys  
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 Arg Ser Gln Pro Gln His Phe Thr Tyr His Pro Val Pro Ala Ile Lys  
 915 920 925  
 Thr Glu Pro Thr Asp Glu Tyr Asp Pro Thr Leu Ile Cys Ser Pro Thr  
 930 935 940  
 His Gly Gly Leu Gly Ser Gln Pro Tyr Tyr Pro Gln His Pro Met Val  
 945 950 955 960  
 Ala Glu Ser Pro Ser Cys Leu Val Ala Thr Met Ala Pro Cys Gln Gln  
 965 970 975  
 Phe Arg Thr Gly Leu Ser Ser Pro Asp Ala Arg Tyr Gln Gln Asn  
 980 985 990  
 Pro Ala Ala Val Leu Tyr Gln Arg Ser Lys Ser Leu Ser Pro Ser Leu  
 995 1000 1005  
 Leu Gly Tyr Gln Gln Pro Ala Leu Met Ala Ala Pro Leu Ser Leu  
 1010 1015 1020  
 Ala Asp Ala His Arg Ser Val Leu Val His Ala Gly Ser Gln Gly  
 1025 1030 1035  
 Gln Ser Ser Ala Leu Leu His Pro Ser Pro Thr Asn Gln Gln Ala  
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 Ser Pro Val Ile His Tyr Ser Pro Thr Asn Gln Gln Leu Arg Cys  
 1055 1060 1065  
 Gly Ser His Gln Glu Phe Gln His Ile Met Tyr Cys Glu Asn Phe  
 1070 1075 1080  
 Ala Pro Gly Thr Thr Arg Pro Gly Pro Pro Pro Val Ser Gln Gly

1085	Gln Arg Leu Ser Pro Gly	1090	Tyr Pro Thr Val	1095	Ile Gln Gln Gln
1100	Asn Ala Thr Ser Gln Arg	1105	Ala Ala Lys Asn Gly	1110	Pro Pro Val Ser
1115	Asp Gln Lys Glu Val Leu	1120	Pro Ala Gly Val Thr	1125	Ile Lys Gln Glu
1130	Gln Asn Leu Asp Gln Thr	1135	Tyr Leu Asp Asp Val	1140	Asn Glu Ile Ile
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<210> 132

<211> 3546

<212> DNA

<213> Artificial Sequence

<220>

<223> NFAT-EGFP fusion

<220>

<221> CDS

<222> (1)..(3543)

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Gly His Glu Pro Gly Gly Ser Pro Gln Asp Glu Leu Asp Phe Ser Ile		
20 25 30		
ctc ttc gac tat gag tat ttg aat ccg aac gaa gaa gag ccg aat gca		144
Leu Phe Asp Tyr Glu Tyr Leu Asn Pro Asn Glu Glu Glu Pro Asn Ala		
35 40 45		
cat aag gtc gcc agc cca ccc tcc gga ccc gca tac ccc gat gat gta		192
His Lys Val Ala Ser Pro Pro Ser Gly Pro Ala Tyr Pro Asp Asp Val		
50 55 60		
atg gac tat ggc ctc aag cca tac agc ccc ctt gct agt ctc tct ggc		240
Met Asp Tyr Gly Leu Lys Pro Tyr Ser Pro Leu Ala Ser Leu Ser Gly		
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Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp Arg Val Gly Pro Gln Lys		
85 90 95		
ttt ctg agc gcg gcc aag cca gca ggg gcc tcg ggc ctg agc cct cgg		336
Phe Leu Ser Ala Ala Lys Pro Ala Gly Ala Ser Gly Leu Ser Pro Arg		
100 105 110		
atc gag atc act ccg tcc cac gaa ctg atc cag gca gtg ggg ccc ctc		384
Ile Glu Ile Thr Pro Ser His Glu Leu Ile Gln Ala Val Gly Pro Leu		
115 120 125		
cgc atg aga gac gcg ggc ctc ctg gtg gag cag cct ccc ctg gcc ggg		432
Arg Met Arg Asp Ala Gly Leu Leu Val Glu Gln Pro Pro Leu Ala Gly		
130 135 140		

gtg gcc gcc agc ccg agg ttc acc ctg ccc gtg ccc ggc ttc gag ggc	480
Val Ala Ala Ser Pro Arg Phe Thr Leu Pro Val Pro Gly Phe Glu Gly	
145 150 155 160	
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Tyr Arg Glu Pro Leu Cys Leu Ser Pro Ala Ser Ser Gly Ser Ser Ala	
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Ser Phe Ile Ser Asp Thr Phe Ser Pro Tyr Thr Ser Pro Cys Val Ser	
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Pro Asn Asn Gly Gly Pro Asp Asp Leu Cys Pro Gln Phe Gln Asn Ile	
195 200 205	
cct gct cat tat tcc ccc aga acc tcg cca ata atg tca cct cga acc	672
Pro Ala His Tyr Ser Pro Arg Thr Ser Pro Ile Met Ser Pro Arg Thr	
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Ser Leu Ala Glu Asp Ser Cys Leu Gly Arg His Ser Pro Val Pro Arg	
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Pro Ala Ser Arg Ser Ser Ser Pro Gly Ala Lys Arg Arg His Ser Cys	
245 250 255	
gcc gag gcc ttg gtt gcc ctg ccg ccc gga gcc tca ccc cag cgc tcc	816
Ala Glu Ala Leu Val Ala Leu Pro Pro Gly Ala Ser Pro Gln Arg Ser	
260 265 270	
cgg agc ccc tcg ccg cag ccc tca tct cac gtg gca ccc cag gac cac	864
Arg Ser Pro Ser Pro Gln Pro Ser Ser His Val Ala Pro Gln Asp His	
275 280 285	
ggc tcc ccg gct ggg tac ccc cct gtg gct ggc tct gcc gtg atc atg	912
Gly Ser Pro Ala Gly Tyr Pro Pro Val Ala Gly Ser Ala Val Ile Met	
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Asp Ala Leu Asn Ser Leu Ala Thr Asp Ser Pro Cys Gly Ile Pro Pro	
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Lys Met Trp Lys Thr Ser Pro Asp Pro Ser Pro Val Ser Ala Ala Pro	
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Ser Lys Ala Gly Leu Pro Arg His Ile Tyr Pro Ala Val Glu Phe Leu	
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Gly Pro Cys Glu Gln Gly Glu Arg Arg Asn Ser Ala Pro Glu Ser Ile	
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Leu Leu Val Pro Pro Thr Trp Pro Lys Pro Leu Val Pro Ala Ile Pro	
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Ile Cys Ser Ile Pro Val Thr Ala Ser Leu Pro Pro Leu Glu Trp Pro	
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Lys Pro His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg Gly Ala	
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Val Lys Ala Pro Thr Gly Gly His Pro Val Val Gln Leu His Gly Tyr	
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Glu Arg Ile Leu Lys Pro His Ala Phe Tyr Gln Val His Arg Ile Thr	
465 470 475 480	

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Gly	Lys	Thr	Val	Thr	Thr	Thr	Ser	Tyr	Glu	Lys	Ile	Val	Gly	Asn	Thr	
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Lys	Val	Leu	Glu	Ile	Pro	Leu	Glu	Pro	Lys	Asn	Asn	Met	Arg	Ala	Thr	
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Ile	Asp	Cys	Ala	Gly	Ile	Leu	Lys	Leu	Arg	Asn	Ala	Asp	Ile	Glu	Leu	
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Arg	Lys	Gly	Glu	Thr	Asp	Ile	Gly	Arg	Lys	Asn	Thr	Arg	Val	Arg	Leu	
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Val	Phe	Arg	Val	His	Ile	Pro	Glu	Ser	Ser	Gly	Arg	Ile	Val	Ser	Leu	
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Gln	Thr	Ala	Ser	Asn	Pro	Ile	Glu	Cys	Ser	Gln	Arg	Ser	Ala	His	Glu	
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Leu	Pro	Met	Val	Glu	Arg	Gln	Asp	Thr	Asp	Ser	Cys	Leu	Val	Tyr	Gly	
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Gly	Gln	Gln	Met	Ile	Leu	Thr	Gly	Gln	Asn	Phe	Thr	Ser	Glu	Ser	Lys	
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Val	Val	Phe	Thr	Glu	Lys	Thr	Thr	Asp	Gly	Gln	Gln	Ile	Trp	Glu	Met	
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gaa	gcc	acg	gtg	gat	aag	gac	aag	agc	cag	ccc	aac	atg	ctt	ttt	gtt	1920
Glu	Ala	Thr	Val	Asp	Lys	Asp	Lys	Ser	Gln	Pro	Asn	Met	Leu	Phe	Val	
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gag	atc	cct	gaa	tat	cgg	aac	aag	cat	atc	cgc	aca	cct	gta	aaa	gtg	1968
Glu	Ile	Pro	Glu	Tyr	Arg	Asn	Lys	His	Ile	Arg	Thr	Pro	Val	Lys	Val	
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aac	ttc	tac	gtc	atc	aat	ggg	aag	aga	aaa	cga	agt	cag	cct	cag	cac	2016
Asn	Phe	Tyr	Val	Ile	Asn	Gly	Lys	Arg	Lys	Arg	Ser	Gln	Pro	Gln	His	
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Phe	Thr	Tyr	His	Pro	Val	Pro	Ala	Ile	Lys	Thr	Glu	Pro	Thr	Asp	Glu	
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Tyr	Asp	Pro	Thr	Leu	Ile	Cys	Ser	Pro	Thr	His	Gly	Gly	Leu	Gly	Ser	
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cag	cct	tac	tac	ccc	cag	cac	ccg	atg	gtg	gcc	gag	tcc	ccc	tcc	tgc	2160
Gln	Pro	Tyr	Tyr	Pro	Gln	His	Pro	Met	Val	Ala	Glu	Ser	Pro	Ser	Cys	
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ctc	gtg	gcc	acc	atg	gct	ccc	tgc	cag	cag	ttc	cgc	acg	ggg	ctc	tca	2208
Leu	Val	Ala	Thr	Met	Ala	Pro	Cys	Gln	Gln	Phe	Arg	Thr	Gly	Leu	Ser	
				725					730					735		
tcc	cct	gac	gcc	cgc	tac	cag	caa	cag	aac	cca	gcg	gcc	gta	ctc	tac	2256
Ser	Pro	Asp	Ala	Arg	Tyr	Gln	Gln	Gln	Asn	Pro	Ala	Ala	Val	Leu	Tyr	
			740					745				750				
cag	cgg	agc	aag	agc	ctg	agc	ccc	agc	ctg	ctg	ggc	tat	cag	cag	ccg	2304
Gln	Arg	Ser	Lys	Ser	Leu	Ser	Pro	Ser	Leu	Leu	Gly	Tyr	Gln	Gln	Pro	
			755				760					765				
gcc	ctc	atg	gcc	gcc	ccg	ctg	tcc	ctt	gcg	gac	gct	cac	cgc	tct	gtg	2352
Ala	Leu	Met	Ala	Ala	Pro	Leu	Ser	Leu	Ala	Asp	Ala	His	Arg	Ser	Val	
			770			775					780					
ctg	gtg	cac	gcc	ggc	tcc	cag	ggc	cag	agc	tca	gcc	ctg	ctc	cac	ccc	2400
Leu	Val	His	Ala	Gly	Ser	Gln	Gly	Gln	Ser	Ser	Ala	Leu	Leu	His	Pro	
					790					795					800	
tct	ccg	acc	aac	cag	cag	gcc	tcg	cct	gtg	atc	cac	tac	tca	ccc	acc	2448
Ser	Pro	Thr	Asn	Gln	Gln	Ala	Ser	Pro	Val	Ile	His	Tyr	Ser	Pro	Thr	
				805					810					815		

aac cag cag ctg cgc tgc gga agc cac cag gag ttc cag cac atc atg	2496
Asn Gln Gln Leu Arg Cys Gly Ser His Gln Glu Phe Gln His Ile Met	
820 825 830	
tac tgc gag aat ttc gca cca ggc acc acc aga cct ggc ccg ccc ccg	2544
Tyr Cys Glu Asn Phe Ala Pro Gly Thr Thr Arg Pro Gly Pro Pro Pro	
835 840 845	
gtc agt caa ggt cag agg ctg agc ccg ggt tcc tac ccc aca gtc att	2592
Val Ser Gln Gly Gln Arg Leu Ser Pro Gly Ser Tyr Pro Thr Val Ile	
850 855 860	
cag cag cag aat gcc acg agc caa aga gcc gcc aaa aac gga ccc ccg	2640
Gln Gln Gln Asn Ala Thr Ser Gln Arg Ala Ala Lys Asn Gly Pro Pro	
865 870 875 880	
gtc agt gac caa aag gaa gta tta cct gcg ggg gtg acc att aaa cag	2688
Val Ser Asp Gln Lys Glu Val Leu Pro Ala Gly Val Thr Ile Lys Gln	
885 890 895	
gag cag aac ttg gac cag acc tac ttg gat gat gtt aat gaa att atc	2736
Glu Gln Asn Leu Asp Gln Thr Tyr Leu Asp Asp Val Asn Glu Ile Ile	
900 905 910	
agg aag gag ttt tca gga cct cct gcc aga aat cag acg aga att ctg	2784
Arg Lys Glu Phe Ser Gly Pro Pro Ala Arg Asn Gln Thr Arg Ile Leu	
915 920 925	
cag tgc acg gta ccg cgg gcc cgg gat cca ccg gtc gcc acc atg gtg	2832
Gln Ser Thr Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met Val	
930 935 940	
agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag	2880
Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu	
945 950 955 960	
ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc	2928
Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly	
965 970 975	
gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc	2976
Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr	
980 985 990	
acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc	3024
Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr	
995 1000 1005	
tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag	3069
Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
1010 1015 1020	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	3114
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
1025 1030 1035	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc	3159
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala	
1040 1045 1050	
gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg	3204
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu	
1055 1060 1065	
aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag	3249
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys	
1070 1075 1080	
ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc gac	3294
Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp	
1085 1090 1095	
aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac	3339
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn	
1100 1105 1110	
atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac	3384
Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn	
1115 1120 1125	
acc ccc atc ggc gac ggc gtg ctg ctg ccc gac aac cac tac	3429
Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr	
1130 1135 1140	

ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc	3474
Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg	
1145 1150 1155	
gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act	3519
Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr	
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ctc ggc atg gac gag ctg tac aag taa	3546
Leu Gly Met Asp Glu Leu Tyr Lys	
1175 1180	

<210> 133

<211> 1181

<212> PRT

<213> Artificial Sequence

<220>

<223> NFAT-EGFP fusion

<400> 133

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Leu Phe Asp Tyr Glu Tyr Leu Asn Pro Asn Glu Glu Glu Pro Asn Ala	
35 40 45	
His Lys Val Ala Ser Pro Pro Ser Gly Pro Ala Tyr Pro Asp Asp Val	
50 55 60	
Met Asp Tyr Gly Leu Lys Pro Tyr Ser Pro Leu Ala Ser Leu Ser Gly	
65 70 75 80	
Glu Pro Pro Gly Arg Phe Gly Glu Pro Asp Arg Val Gly Pro Gln Lys	
85 90 95	
Phe Leu Ser Ala Ala Lys Pro Ala Gly Ala Ser Gly Leu Ser Pro Arg	
100 105 110	
Ile Glu Ile Thr Pro Ser His Glu Leu Ile Gln Ala Val Gly Pro Leu	
115 120 125	
Arg Met Arg Asp Ala Gly Leu Val Glu Gln Pro Pro Leu Ala Gly	
130 135 140	
Val Ala Ala Ser Pro Arg Phe Thr Leu Pro Val Pro Gly Phe Glu Gly	
145 150 155 160	
Tyr Arg Glu Pro Leu Cys Leu Ser Pro Ala Ser Ser Gly Ser Ser Ala	
165 170 175	
Ser Phe Ile Ser Asp Thr Phe Ser Pro Tyr Thr Ser Pro Cys Val Ser	
180 185 190	
Pro Asn Asn Gly Gly Pro Asp Asp Leu Cys Pro Gln Phe Gln Asn Ile	
195 200 205	
Pro Ala His Tyr Ser Pro Arg Thr Ser Pro Ile Met Ser Pro Arg Thr	
210 215 220	
Ser Leu Ala Glu Asp Ser Cys Leu Gly Arg His Ser Pro Val Pro Arg	
225 230 235 240	
Pro Ala Ser Arg Ser Ser Ser Pro Gly Ala Lys Arg Arg His Ser Cys	
245 250 255	
Ala Glu Ala Leu Val Ala Leu Pro Pro Gly Ala Ser Pro Gln Arg Ser	
260 265 270	
Arg Ser Pro Ser Pro Gln Pro Ser Ser His Val Ala Pro Gln Asp His	
275 280 285	
Gly Ser Pro Ala Gly Tyr Pro Pro Val Ala Gly Ser Ala Val Ile Met	



290	Asp	Ala	Leu	Asn	Ser	Leu	295	Ala	Thr	Asp	Ser	Pro	300	Cys	Gly	Ile	Pro	Pro
305	Lys	Met	Trp	Lys	Thr	Ser	310	Pro	Asp	Pro	Ser	Pro	315	Val	Ser	Ala	Ala	Pro
							325	Arg	His	Ile	Tyr	Pro	330	Ala	Val	Glu	Phe	Leu
	Ser	Lys	Ala	Gly	Leu	Pro												
							340	Glu	Arg	Asn	Ser	Ala		Pro	Glu	Ser	Ile	
	Gly	Pro	Cys	Glu	Gln	Gly		Glu	Arg									
							355	Thr	Trp	Pro	Lys	Pro	Leu	Val	Pro	Ala	Ile	Pro
	Leu	Leu	Val	Pro	Pro	Thr												
							370											
							375	Thr	Ala	Ser	Leu	Pro	380	Pro	Leu	Glu	Trp	Pro
	Ile	Cys	Ser	Ile	Pro	Val												
							390	Gly	Ser	Tyr	Glu	Leu	395	Ile	Glu	Val	Gln	Pro
	Leu	Ser	Ser	Gln	Ser													
							405											
							410	Thr	Glu	Thr	Glu	Gly		Ser	Arg	Gly	Ala	
	Lys	Pro	His	His	Arg	Ala		His	Tyr									
							420											
							425											
	Val	Lys	Ala	Pro	Thr	Gly		Gly	His	Pro	Val	Val		Gln	Leu	His	Gly	Tyr
							435											
							440											
	Met	Glu	Asn	Lys	Pro	Leu		Gly	Leu	Gln	Ile	Phe		Ile	Gly	Thr	Ala	Asp
							450											
							455											
	Glu	Arg	Ile	Leu	Lys	Pro		His	Ala	Phe	Tyr	Gln		Val	His	Arg	Ile	Thr
							465											
							470											
	Gly	Lys	Thr	Val	Thr	Thr		Ser	Tyr	Glu	Lys	Ile		Val	Gly	Asn	Thr	
							485											
							490											
	Lys	Val	Leu	Glu	Ile	Pro		Leu	Glu	Pro	Lys	Asn	Asn	Met	Arg	Ala	Thr	
							500											
							505											
	Ile	Asp	Cys	Ala	Gly	Ile		Leu	Lys	Leu	Arg	Asn	Ala	Asp	Ile	Glu	Leu	
							515											
							520											
	Arg	Lys	Gly	Glu	Thr	Asp		Ile	Gly	Arg	Lys	Asn	Thr	Arg	Val	Arg	Leu	
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							535											
	Val	Phe	Arg	Val	His	Ile		Pro	Glu	Ser	Ser	Gly		Arg	Ile	Val	Ser	Leu
							545											
							550											
	Gln	Thr	Ala	Ser	Asn	Pro		Ile	Glu	Cys	Ser	Gln	Arg	Ser	Ala	His	Glu	
							565											
							570											
	Leu	Pro	Met	Val	Glu	Arg		Gln	Asp	Thr	Asp	Ser	Cys	Leu	Val	Tyr	Gly	
							580											
							585											
	Gly	Gln	Gln	Met	Ile	Leu		Thr	Gly	Gln	Asn	Phe	Thr	Ser	Glu	Ser	Lys	
							595											
							600											
	Val	Val	Phe	Thr	Glu	Lys		Thr	Thr	Asp	Gly	Gln	Gln	Ile	Trp	Glu	Met	
							610											
							615											
	Glu	Ala	Thr	Val	Asp	Lys		Asp	Lys	Ser	Gln	Pro	Asn	Met	Leu	Phe	Val	
							625											
	Glu	Ile	Pro	Glu	Tyr	Arg		Asn	Lys	His	Ile	Arg	Thr	Pro	Val	Lys	Val	
							630											
							645											
	Asn	Phe	Tyr	Val	Ile	Asn		Gly	Lys	Arg	Lys	Arg	Ser	Gln	Pro	Gln	His	
							660											
							665											
	Phe	Thr	Tyr	His	Pro	Val		Pro	Ala	Ile	Lys	Thr	Glu	Pro	Thr	Asp	Glu	
							675											
							680											
	Tyr	Asp	Pro	Thr	Leu	Ile		Cys	Ser	Pro	Thr	His	Gly	Gly	Leu	Gly	Ser	
							690											
							695											
	Gln	Pro	Tyr	Tyr	Pro	Gln		His	Pro	Met	Val	Ala	Glu	Ser	Pro	Ser	Cys	
							705											
							710											
	Leu	Val	Ala	Thr	Met	Ala		Pro	Cys	Gln	Gln	Phe	Arg	Thr	Gly	Leu	Ser	
							725											
							730											
	Ser	Pro	Asp	Ala	Arg	Tyr		Gln	Gln	Gln	Asn	Pro	Ala	Ala	Val	Leu	Tyr	
							740											
							745											
	Gln	Arg	Ser	Lys	Ser	Leu		Ser	Pro	Ser	Leu	Leu	Gly	Tyr	Gln	Gln	Pro	
							755											
							760											
	Ala	Leu	Met	Ala	Ala	Pro		Leu	Ser	Leu	Ala	Asp	Ala	His	Arg	Ser	Val	
							770											
							775											
	Leu	Val	His	Ala	Gly	Ser		Gln	Gly	Gln	Ser	Ser	Ala	Leu	Leu	His	Pro	
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							795											
							800											



<220>

<223> EGFP-PKG fusion

<220>

<221> CDS

<222> (1)..(2799)

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1          5          10          15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20          25          30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35          40          45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50          55          60
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag      240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65          70          75          80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85          90          95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100          105          110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115          120          125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130          135          140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145          150          155          160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc      528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165          170          175
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc      576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180          185          190
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg      624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195          200          205
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc      672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210          215          220
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc      720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225          230          235          240
gga ctc aga tct cga ggg agc atg ggc acc ttg cgg gat tta cag tac      768
Gly Leu Arg Ser Arg Gly Ser Met Gly Thr Leu Arg Asp Leu Gln Tyr
245          250          255
gcg ctc cag gag aag atc gag gag ctg agg cag cgg gat gct ctc atc      816
Ala Leu Gln Glu Lys Ile Glu Glu Leu Arg Gln Arg Asp Ala Leu Ile
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	260	265	270	
gac gag ctg gag ctg gag ttg gat cag aag gac gaa ctg atc cag aag				864
Asp Glu Leu Glu Leu Glu Leu Asp Gln Lys Asp Glu Leu Ile Gln Lys				
	275	280	285	
ctg cag aac gag ctg gac aag tac cgc tcg gtg atc cga cca gcc acc				912
Leu Gln Asn Glu Leu Asp Lys Tyr Arg Ser Val Ile Arg Pro Ala Thr				
	290	295	300	
cag cag gcg cag aag cag agc gcg agc acc ttg cag ggc gag ccg cgc				960
Gln Gln Ala Gln Lys Gln Ser Ala Ser Thr Leu Gln Gly Glu Pro Arg				
	305	310	315	
acc aag cgc cag gcg atc tcc gcc gag ccc acc gcc ttc gac atc cag				1008
Thr Lys Arg Gln Ala Ile Ser Ala Glu Pro Thr Ala Phe Asp Ile Gln				
	325	330	335	
gat ctc agc cat gtg acc ctg ccc ttc tac ccc aag agc cca cag tcc				1056
Asp Leu Ser His Val Thr Leu Pro Phe Tyr Pro Lys Ser Pro Gln Ser				
	340	345	350	
aag gat ctt ata aag gaa gct atc ctt gac aat gac ttt atg aag aac				1104
Lys Asp Leu Ile Lys Glu Ala Ile Leu Asp Asn Asp Phe Met Lys Asn				
	355	360	365	
ttg gag ctg tcg cag atc cag gag att gtg gat tgt atg tac ccg gtg				1152
Leu Glu Leu Ser Gln Ile Gln Glu Ile Val Asp Cys Met Tyr Pro Val				
	370	375	380	
gag tat ggc aag gac agt tgc atc atc aaa gaa gga gac gtg ggg tca				1200
Glu Tyr Gly Lys Asp Ser Cys Ile Ile Lys Glu Gly Asp Val Gly Ser				
	385	390	395	
ctg gtg tat gtc atg gaa gat ggt aag gtt gaa gtt aca aaa gaa ggt				1248
Leu Val Tyr Val Met Glu Asp Gly Lys Val Glu Val Thr Lys Glu Gly				
	405	410	415	
gtg aag ttg tgt acc atg ggt cca gga aaa gtg ttt ggg gaa ttg gct				1296
Val Lys Leu Cys Thr Met Gly Pro Gly Lys Val Phe Gly Glu Leu Ala				
	420	425	430	
att ctt tac aac tgt acc cgg aca gcg acc gtc aag act ctt gta aat				1344
Ile Leu Tyr Asn Cys Thr Arg Thr Ala Thr Val Lys Thr Leu Val Asn				
	435	440	445	
gta aaa ctc tgg gcc att gat cga caa tgt ttt caa aca ata atg atg				1392
Val Lys Leu Trp Ala Ile Asp Arg Gln Cys Phe Gln Thr Ile Met Met				
	450	455	460	
agg aca gga ctc atc aag cat acc gag tat atg gaa ttt tta aaa agc				1440
Arg Thr Gly Leu Ile Lys His Thr Glu Tyr Met Glu Phe Leu Lys Ser				
	465	470	475	
gtt cca aca ttc cag agc ctt cct gaa gag atc ctc agc aag ctt gct				1488
Val Pro Thr Phe Gln Ser Leu Pro Glu Glu Ile Leu Ser Lys Leu Ala				
	485	490	495	
gat gtc ctt gaa gag acc cac tat gaa aat gga gaa tat att atc agg				1536
Asp Val Leu Glu Thr His Tyr Glu Asn Gly Glu Tyr Ile Ile Arg				
	500	505	510	
caa ggt gca aga ggg gac acc ttc ttt atc atc agc aaa gga acg gta				1584
Gln Gly Ala Arg Gly Asp Thr Phe Phe Ile Ile Ser Lys Gly Thr Val				
	515	520	525	
aat gtc act cgt gaa gac tca ccg agt gaa gac cca gtc ttt ctt aga				1632
Asn Val Thr Arg Glu Asp Ser Pro Ser Glu Asp Pro Val Phe Leu Arg				
	530	535	540	
act tta gga aaa gga gac tgg ttt gga gag aaa gcc ttg cag ggg gaa				1680
Thr Leu Gly Lys Gly Asp Trp Phe Gly Glu Lys Ala Leu Gln Gly Glu				
	545	550	555	
gat gtg aga aca gca aac gta att gct gca gaa gct gta acc tgc ctt				1728
Asp Val Arg Thr Ala Asn Val Ile Ala Glu Ala Val Thr Cys Leu				
	565	570	575	
gtg att gac aga gac tct ttt aaa cat ttg att gga ggg ctg gat gat				1776
Val Ile Asp Arg Asp Ser Phe Lys His Leu Ile Gly Gly Leu Asp Asp				
	580	585	590	
gtt tct aat aaa gca tat gaa gat gca gaa gct aaa gca aaa tat gaa				1824
Val Ser Asn Lys Ala Tyr Glu Asp Ala Glu Ala Lys Ala Lys Tyr Glu				



&lt;210&gt; 135

&lt;211&gt; 933

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; EGFP-PKG fusion

&lt;400&gt; 135

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20     25     30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35     40     45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50     55     60
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65     70     75     80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85     90     95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100    105    110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115    120    125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130    135    140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145    150    155    160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165    170    175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180    185    190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195    200    205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210    215    220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
225    230    235    240
Gly Leu Arg Ser Arg Gly Ser Met Gly Thr Leu Arg Asp Leu Gln Tyr
245    250    255
Ala Leu Gln Glu Lys Ile Glu Glu Leu Arg Gln Arg Asp Ala Leu Ile
260    265    270
Asp Glu Leu Glu Leu Glu Leu Asp Gln Lys Asp Glu Leu Ile Gln Lys
275    280    285
Leu Gln Asn Glu Leu Asp Lys Tyr Arg Ser Val Ile Arg Pro Ala Thr
290    295    300
Gln Gln Ala Gln Lys Gln Ser Ala Ser Thr Leu Gln Gly Glu Pro Arg
305    310    315    320
Thr Lys Arg Gln Ala Ile Ser Ala Glu Pro Thr Ala Phe Asp Ile Gln
325    330    335
Asp Leu Ser His Val Thr Leu Pro Phe Tyr Pro Lys Ser Pro Gln Ser
340    345    350
Lys Asp Leu Ile Lys Glu Ala Ile Leu Asp Asn Asp Phe Met Lys Asn

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Leu Gly Asn Leu Lys Asn Gly Val Lys Asp Ile Gln Lys His Lys Trp  
 865 870 875 880  
 Phe Glu Gly Phe Asn Trp Glu Gly Leu Arg Lys Gly Thr Leu Thr Pro  
 885 890 895  
 Pro Ile Ile Pro Ser Val Ala Ser Pro Thr Asp Thr Ser Asn Phe Asp  
 900 905 910  
 Ser Phe Pro Glu Asp Asn Asp Glu Pro Pro Pro Asp Asp Asn Ser Gly  
 915 920 925  
 Trp Asp Ile Asp Phe  
 930

<210> 136

<211> 2799

<212> DNA

<213> Artificial Sequence

<220>

<223> PKG-EGFP fusion

<220>

<221> CDS

<222> (1)..(2796)

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 Glu Leu Arg Gln Arg Asp Ala Leu Ile Asp Glu Leu Glu Leu Glu Leu  
 20 25 30  
 gat cag aag gac gaa ctg atc cag aag ctg cag aac gag ctg gac aag 144  
 Asp Gln Lys Asp Glu Leu Ile Gln Lys Leu Gln Asn Glu Leu Asp Lys  
 35 40 45  
 tac cgc tcg gtg atc cga cca gcc acc cag cag gcg cag aag cag agc 192  
 Tyr Arg Ser Val Ile Arg Pro Ala Thr Gln Gln Ala Gln Lys Gln Ser  
 50 55 60  
 gcg agc acc ttg cag ggc gag ccg cgc acc aag cgg cag gcg atc tcc 240  
 Ala Ser Thr Leu Gln Gly Glu Pro Arg Thr Lys Arg Gln Ala Ile Ser  
 65 70 75 80  
 gcc gag ccc acc gcc ttc gac atc cag gat ctc agc cat gtg acc ctg 288  
 Ala Glu Pro Thr Ala Phe Asp Ile Gln Asp Leu Ser His Val Thr Leu  
 85 90 95  
 ccc ttc tac ccc aag agc cca cag tcc aag gat ctt ata aag gaa gct 336  
 Pro Phe Tyr Pro Lys Ser Pro Gln Ser Lys Asp Leu Ile Lys Glu Ala  
 100 105 110  
 atc ctt gac aat gac ttt atg aag aac ttg gag ctg tcg cag atc cag 384  
 Ile Leu Asp Asn Asp Phe Met Lys Asn Leu Glu Leu Ser Gln Ile Gln  
 115 120 125  
 gag att gtg gat tgt atg tac ccg gtg gag tat ggc aag gac agt tgc 432  
 Glu Ile Val Asp Cys Met Tyr Pro Val Glu Tyr Gly Lys Asp Ser Cys  
 130 135 140  
 atc atc aaa gaa gga gac gtg ggg tca ctg gtg tat gtc atg gaa gat 480



Ile 145	Ile	Lys	Glu	Gly	Asp 150	Val	Gly	Ser	Leu	Val 155	Tyr	Val	Met	Glu	Asp 160	
ggt	aag	gtt	gaa	gtt	aca	aaa	gaa	ggt	gtg	aag	ttg	tgt	acc	atg	ggt	528
Gly	Lys	Val	Glu	Val	Thr	Lys	Glu	Gly	Val	Lys	Leu	Cys	Thr	Met	Gly	
				165					170						175	
cca	gga	aaa	gtg	ttt	ggg	gaa	ttg	gct	att	ctt	tac	aac	tgt	acc	cgg	576
Pro	Gly	Lys	Val	Phe	Gly	Glu	Leu	Ala	Ile	Leu	Tyr	Asn	Cys	Thr	Arg	
				180					185						190	
aca	gcg	acc	gtc	aag	act	ctt	gta	aat	gta	aaa	ctc	tgg	gcc	att	gat	624
Thr	Ala	Thr	Val	Lys	Thr	Leu	Val	Asn	Val	Lys	Leu	Trp	Ala	Ile	Asp	
				195					200						205	
cga	caa	tgt	ttt	caa	aca	ata	atg	atg	agg	aca	gga	ctc	atc	aag	cat	672
Arg	Gln	Cys	Phe	Gln	Thr	Ile	Met	Met	Arg	Thr	Gly	Leu	Ile	Lys	His	
						210									220	
acc	gag	tat	atg	gaa	ttt	tta	aaa	agc	gtt	cca	aca	ttc	cag	agc	ctt	720
Thr	Glu	Tyr	Met	Glu	Phe	Leu	Lys	Ser	Val	Pro	Thr	Phe	Gln	Ser	Leu	
225						230									240	
cct	gaa	gag	atc	ctc	agc	aag	ctt	gct	gat	gtc	ctt	gaa	gag	acc	cac	768
Pro	Glu	Glu	Ile	Leu	Ser	Lys	Leu	Ala	Asp	Val	Leu	Glu	Glu	Thr	His	
						245									255	
tat	gaa	aat	gga	gaa	tat	att	atc	agg	caa	ggg	gca	aga	ggg	gac	acc	816
Tyr	Glu	Asn	Gly	Glu	Tyr	Ile	Ile	Arg	Gln	Gly	Ala	Arg	Gly	Asp	Thr	
						260									270	
ttc	ttt	atc	atc	agc	aaa	gga	acg	gta	aat	gtc	act	cgt	gaa	gac	tca	864
Phe	Phe	Ile	Ile	Ser	Lys	Gly	Thr	Val	Asn	Val	Thr	Arg	Glu	Asp	Ser	
						275									285	
ccg	agt	gaa	gac	cca	gtc	ttt	ctt	aga	act	tta	gga	aaa	gga	gac	tggt	912
Pro	Ser	Glu	Asp	Pro	Val	Phe	Leu	Arg	Thr	Leu	Gly	Lys	Gly	Asp	Trp	
290						295									300	
ttt	gga	gag	aaa	gcc	ttg	cag	ggg	gaa	gat	gtg	aga	aca	gca	aac	gta	960
Phe	Gly	Glu	Lys	Ala	Gln	Gly	Glu	Asp	Val	Arg	Thr	Ala	Asn	Val		
305						310									320	
att	gct	gca	gaa	gct	gta	acc	tgc	ctt	gtg	att	gac	aga	gac	tct	ttt	1008
Ile	Ala	Ala	Glu	Ala	Val	Thr	Cys	Leu	Val	Ile	Asp	Arg	Asp	Ser	Phe	
						325									335	
aaa	cat	ttg	att	gga	ggg	ctg	gat	gat	gtt	tct	aat	aaa	gca	tat	gaa	1056
Lys	His	Leu	Ile	Gly	Gly	Leu	Asp	Val	Ser	Asn	Lys	Ala	Tyr	Glu		
						340									350	
gat	gca	gaa	gct	aaa	gca	aaa	tat	gaa	gct	gaa	gcg	gct	ttc	ttc	gcc	1104
Asp	Ala	Glu	Ala	Lys	Ala	Lys	Tyr	Glu	Ala	Glu	Ala	Ala	Phe	Phe	Ala	
															365	
aac	ctg	aag	ctg	tct	gat	ttc	aac	atc	att	gat	acc	ctt	gga	gtt	gga	1152
Asn	Leu	Lys	Leu	Ser	Asp	Phe	Asn	Ile	Ile	Asp	Thr	Leu	Gly	Val	Gly	
370						375									380	
ggt	ttc	gga	cga	gta	gaa	ctg	gtc	cag	ttg	aaa	agt	gaa	gaa	tcc	aaa	1200
Gly	Phe	Gly	Arg	Val	Glu	Leu	Val	Gln	Leu	Lys	Ser	Glu	Glu	Ser	Lys	
385						390									400	
acg	ttt	gca	atg	aag	att	ctc	aag	aaa	cgt	cac	att	gtg	gac	aca	aga	1248
Thr	Phe	Ala	Met	Lys	Ile	Leu	Lys	Lys	Arg	His	Ile	Val	Asp	Thr	Arg	
						405									415	
cag	cag	gag	cac	atc	cgc	tca	gag	aag	cag	atc	atg	cag	ggg	gct	cat	1296
Gln	Gln	Glu	His	Ile	Arg	Ser	Glu	Lys	Gln	Ile	Met	Gln	Gly	Ala	His	
															420	
tcc	gat	ttc	ata	gtg	aga	ctg	tac	aga	aca	ttt	aag	gac	agc	aaa	tat	1344
Ser	Asp	Phe	Ile	Val	Arg	Leu	Tyr	Arg	Thr	Phe	Lys	Asp	Ser	Lys	Tyr	
						435									445	
ttg	tat	atg	ttg	atg	gaa	gct	tgt	cta	ggg	gga	gag	ctc	tgg	acc	att	1392
Leu	Tyr	Met	Leu	Met	Glu	Ala	Cys	Leu	Gly	Gly	Glu	Leu	Trp	Thr	Ile	
450						455									460	
ctc	agg	gat	aga	ggg	tcg	ttt	gaa	gat	tct	aca	acc	aga	ttt	tac	aca	1440
Leu	Arg	Asp	Arg	Gly	Ser	Phe	Glu	Asp	Ser	Thr	Thr	Arg	Phe	Tyr	Thr	
465						470									480	
gca	tgt	gtg	gta	gaa	gct	ttt	gcc	tat	ctg	cat	tcc	aaa	gga	atc	att	1488

Ala	Cys	Val	Val	Glu	Ala	Phe	Ala	Tyr	Leu	His	Ser	Lys	Gly	Ile	Ile	
485				490										495		
tac	agg	gac	ctc	aag	cca	gaa	aat	ctc	atc	cta	gat	cac	cga	ggg	tat	1536
Tyr	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Leu	Ile	Leu	Asp	His	Arg	Gly	Tyr	
500				505									510			
gcc	aaa	ctg	gtt	gat	ttt	ggc	ttt	gca	aag	aaa	ata	gga	ttt	gga	aag	1584
Ala	Lys	Leu	Val	Asp	Phe	Gly	Phe	Ala	Lys	Lys	Ile	Gly	Phe	Gly	Lys	
515				520									525			
aaa	aca	tgg	act	ttt	tgt	ggg	act	cca	gag	tat	gta	gcc	cca	gag	atc	1632
Lys	Thr	Trp	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Val	Ala	Pro	Glu	Ile	
530				535												
atc	ctg	aac	aaa	ggc	cat	gac	att	tca	gcc	gac	tac	tgg	tca	ctg	gga	1680
Ile	Leu	Asn	Lys	Gly	His	Asp	Ile	Ser	Ala	Asp	Tyr	Trp	Ser	Leu	Gly	
545				550											560	
atc	cta	atg	tat	gaa	ctc	ctg	act	ggc	agc	cca	cct	ttc	tca	ggc	cca	1728
Ile	Leu	Met	Tyr	Glu	Leu	Leu	Thr	Gly	Ser	Pro	Pro	Phe	Ser	Gly	Pro	
565				570												
gat	cct	atg	aaa	acc	tat	aac	atc	ata	ttg	agg	ggg	att	gac	atg	ata	1776
Asp	Pro	Met	Lys	Thr	Tyr	Asn	Ile	Ile	Leu	Arg	Gly	Ile	Asp	Met	Ile	
580				585												
gaa	ttt	cca	aag	aag	att	gcc	aaa	aat	gct	gct	aat	tta	att	aaa	aaa	1824
Glu	Phe	Pro	Lys	Lys	Ile	Ala	Lys	Asn	Ala	Ala	Asn	Leu	Ile	Lys	Lys	
595				600									605			
cta	tgc	agg	gac	aat	cca	tca	gaa	aga	tta	ggg	aat	ttg	aaa	aat	gga	1872
Leu	Cys	Arg	Asp	Asn	Pro	Ser	Glu	Arg	Leu	Gly	Asn	Leu	Lys	Asn	Gly	
610				615												
gta	aaa	gac	att	caa	aag	cac	aaa	tgg	ttt	gag	ggc	ttt	aac	tgg	gaa	1920
Val	Lys	Asp	Ile	Gln	Lys	His	Lys	Trp	Phe	Glu	Gly	Phe	Asn	Trp	Glu	
625				630											640	
ggc	tta	aga	aaa	ggg	acc	ttg	aca	cct	cct	ata	ata	cca	agt	gtt	gca	1968
Gly	Leu	Arg	Lys	Gly	Thr	Leu	Thr	Pro	Pro	Ile	Ile	Pro	Ser	Val	Ala	
645				650											655	
tca	ccc	aca	gac	aca	agt	aat	ttt	gac	agt	ttc	cct	gag	gac	aac	gat	2016
Ser	Pro	Thr	Asp	Thr	Ser	Asn	Phe	Asp	Ser	Phe	Pro	Glu	Asp	Asn	Asp	
660				665												
gaa	cca	cca	cct	gat	gac	aac	tca	gga	tgg	gat	ata	gac	ttc	tcg	gat	2064
Glu	Pro	Pro	Pro	Asp	Asp	Asn	Ser	Gly	Trp	Asp	Ile	Asp	Phe	Ser	Asp	
675				680												
cca	ccg	gtc	gcc	acc	atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	2112
Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	

Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly		
			820					825					830				
cac	aag	ctg	gag	tac	aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	2544	
His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala		
			835				840					845					
gac	aag	cag	aag	aac	ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	2592	
Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn		
			850				855					860					
atc	gag	gac	ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	2640	
Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr		
							870				875				880		
ccc	atc	ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	2688	
Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser		
							885				890				895		
acc	cag	tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	2736	
Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met		
			900					905					910				
gtc	ctg	ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	2784	
Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp		
			915					920					925				
gag	ctg	tac	aag	taa												2799	
Glu	Leu	Tyr	Lys														
			930														

<210> 137

<211> 932

<212> PRT

<213> Artificial Sequence

<220>

<223> PKG-EGFP fusion

<400> 137

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Glu	Leu	Arg	Gln	Arg	Asp	Ala	Leu	Ile	Asp	Glu	Leu	Glu	Leu	Glu	Leu		
			20					25					30				
Asp	Gln	Lys	Asp	Glu	Leu	Ile	Gln	Lys	Leu	Gln	Asn	Glu	Leu	Asp	Lys		
		35					40					45					
Tyr	Arg	Ser	Val	Ile	Arg	Pro	Ala	Thr	Gln	Gln	Ala	Gln	Lys	Gln	Ser		
	50					55					60						
Ala	Ser	Thr	Leu	Gln	Gly	Glu	Pro	Arg	Thr	Lys	Arg	Gln	Ala	Ile	Ser		
					70					75					80		
Ala	Glu	Pro	Thr	Ala	Phe	Asp	Ile	Gln	Asp	Leu	Ser	His	Val	Thr	Leu		
				85					90					95			
Pro	Phe	Tyr	Pro	Lys	Ser	Pro	Gln	Ser	Lys	Asp	Leu	Ile	Lys	Glu	Ala		
			100					105					110				
Ile	Leu	Asp	Asn	Asp	Phe	Met	Lys	Asn	Leu	Glu	Leu	Ser	Gln	Ile	Gln		
		115					120					125					
Glu	Ile	Val	Asp	Cys	Met	Tyr	Pro	Val	Glu	Tyr	Gly	Lys	Asp	Ser	Cys		
		130				135					140						
Ile	Ile	Lys	Glu	Gly	Asp	Val	Gly	Ser	Leu	Val	Tyr	Val	Met	Glu	Asp		
					150					155				160			
Gly	Lys	Val	Glu	Val	Thr	Lys	Glu	Gly	Val	Lys	Leu	Cys	Thr	Met	Gly		
				165					170					175			
Pro	Gly	Lys	Val	Phe	Gly	Glu	Leu	Ala	Ile	Leu	Tyr	Asn	Cys	Thr	Arg		



Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly  
 690 695 700  
 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys  
 705 710 715 720  
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu  
 725 730 735  
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro  
 740 745 750  
 Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr  
 755 760 765  
 Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu  
 770 775 780  
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr  
 785 790 795 800  
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg  
 805 810 815  
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly  
 820 825 830  
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala  
 835 840 845  
 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn  
 850 855 860  
 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr  
 865 870 875 880  
 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser  
 885 890 895  
 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met  
 900 905 910  
 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp  
 915 920 925  
 Glu Leu Tyr Lys  
 930

<210> 138

<211> 2184

<212> DNA

<213> Artificial Sequence

<220>

<223> EGFP-PKB fusion

<220>

<221> CDS

<222> (1)..(2181)

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ctg	acc	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
	65				70					75					80	
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
	145				150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165				170						175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac	ggc	576
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	
			180					185					190			
ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	tcc	gcc	ctg	624
Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	
		195					200					205				
agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	gag	ttc	672
Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	
	210					215					220					
gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	aag	tcc	720
Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	
		225			230					235					240	
gga	ctc	aga	tct	cga	ggc	acc	atg	agc	gac	gtg	gct	att	gtg	aag	gag	768
Gly	Leu	Arg	Ser	Arg	Gly	Thr	Met	Ser	Asp	Val	Ala	Ile	Val	Lys	Glu	
				245					250					255		
ggt	tgg	ctg	cac	aaa	cga	ggg	gag	tac	atc	aag	acc	tgg	cgg	cca	cgc	816
Gly	Trp	Leu	His	Lys	Arg	Gly	Glu	Tyr	Ile	Lys	Thr	Trp	Arg	Pro	Arg	
			260					265					270			
tac	ttc	ctc	ctc	aag	aat	gat	ggc	acc	ttc	att	ggc	tac	aag	gag	cgg	864
Tyr	Phe	Leu	Leu	Lys	Asn	Asp	Gly	Thr	Phe	Ile	Gly	Tyr	Lys	Glu	Arg	
		275					280					285				
ccg	cag	gat	gtg	gac	caa	cgt	gag	gct	ccc	ctc	aac	aac	ttc	tct	gtg	912
Pro	Gln	Asp	Val	Asp	Gln	Arg	Glu	Ala	Pro	Leu	Asn	Asn	Phe	Ser	Val	
		290				295					300					
gcg	cag	tgc	cag	ctg	atg	aag	acg	gag	cgg	ccc	cgg	ccc	aac	acc	ttc	960
Ala	Gln	Cys	Gln	Leu	Met	Lys	Thr	Glu	Arg	Pro	Arg	Pro	Asn	Thr	Phe	
		305				310				315					320	
atc	atc	cgc	tgc	ctg	cag	tgg	acc	act	gtc	atc	gaa	cgc	acc	ttc	cat	1008
Ile	Ile	Arg	Cys	Leu	Gln	Trp	Thr	Thr	Val	Ile	Glu	Arg	Thr	Phe	His	
				325					330					335		
gtg	gag	act	cct	gag	gag	cgg	gag	gag	tgg	aca	acc	gcc	atc	cag	act	1056
Val	Glu	Thr	Pro	Glu	Glu	Arg	Glu	Glu	Trp	Thr	Thr	Ala	Ile	Gln	Thr	
			340					345					350			
gtg	gct	gac	ggc	ctc	aag	aag	cag	gag	gag	gag	gag	atg	gac	ttc	cgg	1104
Val	Ala	Asp	Gly	Leu	Lys	Lys	Gln	Glu	Glu	Glu	Glu	Met	Asp	Phe	Arg	
		355					360					365				

tcg ggc tca ccc agt gac aac tca ggg gct gaa gag atg gag gtg tcc	1152
Ser Gly Ser Pro Ser Asp Asn Ser Gly Ala Glu Glu Met Glu Val Ser	
370 375 380	
ctg gcc aag ccc aag cac cgc gtg acc atg aac gag ttt gag tac ctg	1200
Leu Ala Lys Pro Lys His Arg Val Thr Met Asn Glu Phe Glu Tyr Leu	
385 390 395 400	
aag ctg ctg ggc aag ggc act ttc ggc aag gtg atc ctg gtg aag gag	1248
Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile Leu Val Lys Glu	
405 410 415	
aag gcc aca ggc cgc tac tac gcc atg aag atc ctc aag aag gaa gtc	1296
Lys Ala Thr Gly Arg Tyr Tyr Ala Met Lys Ile Leu Lys Lys Glu Val	
420 425 430	
atc gtg gcc aag gac gag gtg gcc cac aca ctc acc gag aac cgc gtc	1344
Ile Val Ala Lys Asp Glu Val Ala His Thr Leu Thr Glu Asn Arg Val	
435 440 445	
ctg cag aac tcc agg cac ccc ttc ctc aca gcc ctg aag tac tct ttc	1392
Leu Gln Asn Ser Arg His Pro Phe Leu Thr Ala Leu Lys Tyr Ser Phe	
450 455 460	
cag acc cac gac cgc ctc tgc ttt gtc atg gag tac gcc aac ggg ggc	1440
Gln Thr His Asp Arg Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly	
465 470 475 480	
gag ctg ttc ttc cac ctg tcc cgg gaa cgt gtg ttc tcc gag gac cgg	1488
Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe Ser Glu Asp Arg	
485 490 495	
gcc cgc ttc tat ggc gct gag att gtg tca gcc ctg gac tac ctg cac	1536
Ala Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu Asp Tyr Leu His	
500 505 510	
tcg gag aag aac gtg gtg tac cgg gac ctc aag ctg gag aac ctc atg	1584
Ser Glu Lys Asn Val Val Tyr Arg Asp Leu Lys Leu Glu Asn Leu Met	
515 520 525	
ctg gac aag gac ggg cac att aag atc aca gac ttc ggg ctg tgc aag	1632
Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys	
530 535 540	
gag ggg atc aag gac ggt gcc acc atg aag acc ttt tgc ggc aca cct	1680
Glu Gly Ile Lys Asp Gly Ala Thr Met Lys Thr Phe Cys Gly Thr Pro	
545 550 555 560	
gag tac ctg gcc ccc gag gtg ctg gag gac aat gac tac ggc cgt gca	1728
Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala	
565 570 575	
gtg gac tgg tgg ggg ctg ggc gtg gtc atg tac gag atg atg tgc ggt	1776
Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met Met Cys Gly	
580 585 590	
cgc ctg ccc ttc tac aac cag gac cat gag aag ctt ttt gag ctc atc	1824
Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe Glu Leu Ile	
595 600 605	
ctc atg gag gag atc cgc ttc ccg cgc acg ctt ggt ccc gag gcc aag	1872
Leu Met Glu Glu Ile Arg Phe Pro Arg Thr Leu Gly Pro Glu Ala Lys	
610 615 620	
tcc ttg ctt tca ggg ctg ctc aag aag gac ccc aag cag agg ctt ggc	1920
Ser Leu Leu Ser Gly Leu Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly	
625 630 635 640	
ggg ggc tcc gag gac gcc aag gag atc atg cag cat cgc ttc ttt gcc	1968
Gly Gly Ser Glu Asp Ala Lys Glu Ile Met Gln His Arg Phe Phe Ala	
645 650 655	
ggt atc gtg tgg cag cac gtg tac gag aag aag ctc agc cca ccc ttc	2016
Gly Ile Val Trp Gln His Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe	
660 665 670	
aag ccc cag gtc acg tcg gag act gac acc agg tat ttt gat gag gag	2064
Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu	
675 680 685	
ttc acg gcc cag atg atc acc atc aca cca cct gac caa gat gac agc	2112
Phe Thr Ala Gln Met Ile Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser	
690 695 700	

atg gag tgt gtg gac agc gag cgc agg ccc cac ttc ccc cag ttc tcc	2160
Met Glu Cys Val Asp Ser Glu Arg Arg Pro His Phe Pro Gln Phe Ser	
705 710 715 720	
tac tcg gcc agc agc acg gcc tga	2184
Tyr Ser Ala Ser Ser Thr Ala	
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<210> 139

<211> 727

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-PKB fusion

<400> 139

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	
210 215 220	
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser	
225 230 235 240	
Gly Leu Arg Ser Arg Gly Thr Met Ser Asp Val Ala Ile Val Lys Glu	
245 250 255	
Gly Trp Leu His Lys Arg Gly Glu Tyr Ile Lys Thr Trp Arg Pro Arg	
260 265 270	
Tyr Phe Leu Leu Lys Asn Asp Gly Thr Phe Ile Gly Tyr Lys Glu Arg	
275 280 285	
Pro Gln Asp Val Asp Gln Arg Glu Ala Pro Leu Asn Asn Phe Ser Val	
290 295 300	
Ala Gln Cys Gln Leu Met Lys Thr Glu Arg Pro Arg Pro Asn Thr Phe	
305 310 315 320	



Ile	Ile	Arg	Cys	Leu	Gln	Trp	Thr	Thr	Val	Ile	Glu	Arg	Thr	Phe	His		
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Val	Glu	Thr	Pro	Glu	Glu	Arg	Glu	Glu	Trp	Thr	Thr	Ala	Ile	Gln	Thr		
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Val	Ala	Asp	Gly	Leu	Lys	Lys	Gln	Glu	Glu	Glu	Glu	Met	Asp	Phe	Arg		
				355					360					365			
Ser	Gly	Ser	Pro	Ser	Asp	Asn	Ser	Gly	Ala	Glu	Glu	Met	Glu	Val	Ser		
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Leu	Ala	Lys	Pro	Lys	His	Arg	Val	Thr	Met	Asn	Glu	Phe	Glu	Tyr	Leu		
385					390						395				400		
Lys	Leu	Leu	Gly	Lys	Gly	Thr	Phe	Gly	Lys	Val	Ile	Leu	Val	Lys	Glu		
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Lys	Ala	Thr	Gly	Arg	Tyr	Tyr	Ala	Met	Lys	Ile	Leu	Lys	Lys	Glu	Val		
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Ile	Val	Ala	Lys	Asp	Glu	Val	Ala	His	Thr	Leu	Thr	Glu	Asn	Arg	Val		
				435				440					445				
Leu	Gln	Asn	Ser	Arg	His	Pro	Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ser	Phe		
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Gln	Thr	His	Asp	Arg	Leu	Cys	Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly		
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Glu	Leu	Phe	Phe	His	Leu	Ser	Arg	Glu	Arg	Val	Phe	Ser	Glu	Asp	Arg		
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Ala	Arg	Phe	Tyr	Gly	Ala	Glu	Ile	Val	Ser	Ala	Leu	Asp	Tyr	Leu	His		
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Ser	Glu	Lys	Asn	Val	Val	Tyr	Arg	Asp	Leu	Lys	Leu	Glu	Asn	Leu	Met		
				515				520					525				
Leu	Asp	Lys	Asp	Gly	His	Ile	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys		
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Glu	Gly	Ile	Lys	Asp	Gly	Ala	Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro		
545					550					555					560		
Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala		
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Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly		
				580					585					590			
Arg	Leu	Pro	Phe	Tyr	Asn	Gln	Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile		
				595			600						605				
Leu	Met	Glu	Glu	Ile	Arg	Phe	Pro	Arg	Thr	Leu	Gly	Pro	Glu	Ala	Lys		
						615						620					
Ser	Leu	Leu	Ser	Gly	Leu	Leu	Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly		
625					630						635				640		
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Gly	Ile	Val	Trp	Gln	His	Val	Tyr	Glu	Lys	Lys	Leu	Ser	Pro	Pro	Phe		
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Lys	Pro	Gln	Val	Thr	Ser	Glu	Thr	Asp	Thr	Arg	Tyr	Phe	Asp	Glu	Glu		
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Phe	Thr	Ala	Gln	Met	Ile	Thr	Ile	Thr	Pro	Pro	Asp	Gln	Asp	Asp	Ser		
				690		695						700					
Met	Glu	Cys	Val	Asp	Ser	Glu	Arg	Arg	Pro	His	Phe	Pro	Gln	Phe	Ser		
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Tyr	Ser	Ala	Ser	Ser	Thr	Ala											
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<210> 140

<211> 2394

<212> DNA

<213> Artificial Sequence

<220>

<223> NFkappaB-EGFP fusion

<220>

<221> CDS

<222> (1)..(2391)

<400> 140

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tct ggc ccc tat gtg gag atc att gag cag ccc aag cag cgg ggc atg	96
Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met	
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cgc ttc cgc tac aag tgc gag ggg cgc tcc gcg ggc agc atc cca ggc	144
Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly	
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gag agg agc aca gat acc acc aag acc cac ccc acc atc aag atc aat	192
Glu Arg Ser Thr Asp Thr Lys Thr His Pro Thr Ile Lys Ile Asn	
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ggc tac aca gga cca ggg aca gtg cgc atc tcc ctg gtc acc aag gac	240
Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp	
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cct cct cac cgg cct cac ccc cac gag ctt gta gga aag gac tgc cgg	288
Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg	
85 90 95	
gat ggc ttc tat gag gct gag ctc tgc ccg gac cgc tgc atc cac agt	336
Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser	
100 105 110	
ttc cag aac ctg gga atc cag tgt gtg aag aag cgg gac ctg gag cag	384
Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln	
115 120 125	
gct atc agt cag cgc atc cag acc aac aac aac ccc ttc caa gtt cct	432
Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro	
130 135 140	
ata gaa gag cag cgt ggg gac tac gac ctg aat gct gtg cgg ctc tgc	480
Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys	
145 150 155 160	
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Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro	
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Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala	
180 185 190	
gag ctc aag atc tgc cga gtg aac cga aac tct ggc agc tgc ctc ggt	624
Glu Leu Lys Ile Cys Arg Val Asn Arg Asn Ser Gly Ser Cys Leu Gly	
195 200 205	
ggg gat gag atc ttc cta ctg gac aag gtg cag aaa gag gac att	672
Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile	
210 215 220	
gag gtg tat ttc acg gga cca ggc tgg gag gcc cga ggc tcc ttt tcg	720
Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser	
225 230 235 240	
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Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro	
245 250 255	

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Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu	
260 265 270	
cgg cgg cct tcc gac cgg gag ctc agt gag ccc atg gaa ttc cag tac	864
Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr	
275 280 285	
ctg cca gat aca gac gat cgt cac cgg att gag gag aaa cgt aaa agg	912
Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg	
290 295 300	
aca tat gag acc ttc aag agc atc atg aag aag agt cct ttc agc gga	960
Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly	
305 310 315 320	
ccc acc gac ccc cgg cct cca cct cga cgc att gct gtg cct tcc cgc	1008
Pro Thr Asp Pro Arg Pro Pro Pro Arg Ile Ala Val Pro Ser Arg	
325 330 335	
agc tca gct tct gtc ccc aag cca gca ccc cag ccc tat ccc ttt acg	1056
Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr	
340 345 350	
tca tcc ctg agc acc atc aac tat gat gag ttt ccc acc atg gtg ttt	1104
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Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro	
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Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val	
385 390 395 400	
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Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly	
405 410 415	
cct cct cag gct gtg gcc cca cct gcc ccc aag ccc acc cag gct ggg	1296
Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly	
420 425 430	
gaa gga acg ctg tca gag gcc ctg ctg cag ctg cag ttt gat gat gaa	1344
Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu	
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Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln	
465 470 475 480	
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Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr	
485 490 495	
cct gag gct ata act cgc cta gtg aca ggg gcc cag agg ccc ccc gac	1536
Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp	
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Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu	
515 520 525	
tca gga gat gaa gac ttc tcc tcc att gcg gac atg gac ttc tca gcc	1632
Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala	
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Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly	
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Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His	
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Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr	
645 650 655	
atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag	2016
Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys	
660 665 670	
ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac	2064
Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp	
675 680 685	
ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac	2112
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr	
690 695 700	
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Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile	
705 710 715 720	
aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag	2208
Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln	
725 730 735	
ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg	2256
Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val	
740 745 750	
ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa	2304
Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys	
755 760 765	
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Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr	
770 775 780	
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<210> 141

<211> 797

<212> PRT

<213> Artificial Sequence

<220>

<223> NFkappaB-EGFP fusion

<400> 141

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Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly	35	40	45	
Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn				

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Gly	Tyr	Thr	Gly	Pro	Gly	Thr	Val	Arg	Ile	Ser	Leu	Val	Thr	Lys	Asp		
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Pro	Pro	His	Arg	Pro	His	Pro	His	Glu	Leu	Val	Gly	Lys	Asp	Cys	Arg		
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Asp	Gly	Phe	Tyr	Glu	Ala	Glu	Leu	Cys	Pro	Asp	Arg	Cys	Ile	His	Ser		
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Phe	Gln	Asn	Leu	Gly	Ile	Gln	Cys	Val	Lys	Lys	Arg	Asp	Leu	Glu	Gln		
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Ala	Ile	Ser	Gln	Arg	Ile	Gln	Thr	Asn	Asn	Asn	Pro	Phe	Gln	Val	Pro		
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Ile	Glu	Glu	Gln	Arg	Gly	Asp	Tyr	Asp	Leu	Asn	Ala	Val	Arg	Leu	Cys		
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Phe	Gln	Val	Thr	Val	Arg	Asp	Pro	Ser	Gly	Arg	Pro	Leu	Arg	Leu	Pro		
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Pro	Val	Leu	Pro	His	Pro	Ile	Phe	Asp	Asn	Arg	Ala	Pro	Asn	Thr	Ala		
			180					185					190				
Glu	Leu	Lys	Ile	Cys	Arg	Val	Asn	Arg	Asn	Ser	Gly	Ser	Cys	Leu	Gly		
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Gly	Asp	Glu	Ile	Phe	Leu	Leu	Cys	Asp	Lys	Val	Gln	Lys	Glu	Asp	Ile		
210						215					220						
Glu	Val	Tyr	Phe	Thr	Gly	Pro	Gly	Trp	Glu	Ala	Arg	Gly	Ser	Phe	Ser		
225					230				235					240			
Gln	Ala	Asp	Val	His	Arg	Gln	Val	Ala	Ile	Val	Phe	Arg	Thr	Pro	Pro		
				245					250					255			
Tyr	Ala	Asp	Pro	Ser	Leu	Gln	Ala	Pro	Val	Arg	Val	Ser	Met	Gln	Leu		
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Arg	Arg	Pro	Ser	Asp	Arg	Glu	Leu	Ser	Glu	Pro	Met	Glu	Phe	Gln	Tyr		
		275					280					285					
Leu	Pro	Asp	Thr	Asp	Asp	Arg	His	Arg	Ile	Glu	Glu	Lys	Arg	Lys	Arg		
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Thr	Tyr	Glu	Thr	Phe	Lys	Ser	Ile	Met	Lys	Lys	Ser	Pro	Phe	Ser	Gly		
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Pro	Thr	Asp	Pro	Arg	Pro	Pro	Pro	Arg	Arg	Ile	Ala	Val	Pro	Ser	Arg		
				325					330					335			
Ser	Ser	Ala	Ser	Val	Pro	Lys	Pro	Ala	Pro	Gln	Pro	Tyr	Pro	Phe	Thr		
		340						345					350				
Ser	Ser	Leu	Ser	Thr	Ile	Asn	Tyr	Asp	Glu	Phe	Pro	Thr	Met	Val	Phe		
		355					360					365					
Pro	Ser	Gly	Gln	Ile	Ser	Gln	Ala	Ser	Ala	Leu	Ala	Pro	Ala	Pro	Pro		
		370				375					380						
Gln	Val	Leu	Pro	Gln	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Met	Val		
385					390					395				400			
Ser	Ala	Leu	Ala	Gln	Ala	Pro	Ala	Pro	Val	Pro	Val	Leu	Ala	Pro	Gly		
				405					410				415				
Pro	Pro	Gln	Ala	Val	Ala	Pro	Pro	Ala	Pro	Lys	Pro	Thr	Gln	Ala	Gly		
				420				425					430				
Glu	Gly	Thr	Leu	Ser	Glu	Ala	Leu	Leu	Gln	Leu	Gln	Phe	Asp	Asp	Glu		
		435					440				445						
Asp	Leu	Gly	Ala	Leu	Leu	Gly	Asn	Ser	Thr	Asp	Pro	Ala	Val	Phe	Thr		
450						455					460						
Asp	Leu	Ala	Ser	Val	Asp	Asn	Ser	Glu	Phe	Gln	Gln	Leu	Leu	Asn	Gln		
465					470					475				480			
Gly	Ile	Pro	Val	Ala	Pro	His	Thr	Thr	Glu	Pro	Met	Leu	Met	Glu	Tyr		
				485					490					495			
Pro	Glu	Ala	Ile	Thr	Arg	Leu	Val	Thr	Gly	Ala	Gln	Arg	Pro	Pro	Asp		
			500					505					510				
Pro	Ala	Pro	Ala	Pro	Leu	Gly	Ala	Pro	Gly	Leu	Pro	Asn	Gly	Leu	Leu		
		515				520						525					
Ser	Gly	Asp	Glu	Asp	Phe	Ser	Ser	Ile	Ala	Asp	Met	Asp	Phe	Ser	Ala		
		530				535				540							
Leu	Leu	Ser	Gln	Ile	Ser	Ser	Leu	Asp	Pro	Pro	Val	Ala	Thr	Met	Val		
545					550				555					560			

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu  
 565 570 575  
 Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly  
 580 585 590  
 Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr  
 595 600 605  
 Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr  
 610 615 620  
 Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His  
 625 630 635 640  
 Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr  
 645 650 655  
 Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys  
 660 665 670  
 Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp  
 675 680 685  
 Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr  
 690 695 700  
 Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile  
 705 710 715 720  
 Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln  
 725 730 735  
 Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val  
 740 745 750  
 Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys  
 755 760 765  
 Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr  
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 Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 785 790 795

<210> 142

<211> 2394

<212> DNA

<213> Artificial Sequence

<220>

<223> EGFP-NFkappaB fusion

<220>

<221> CDS

<222> (1)..(2391)

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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	

	35		40		45		
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc							192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr							
50		55		60			
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag							240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys							
65		70		75		80	
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag							288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu							
85		90		95			
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag							336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu							
100		105		110			
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc							384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly							
115		120		125			
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac							432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr							
130		135		140			
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac							480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn							
145		150		155		160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc							528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser							
165		170		175			
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc							576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly							
180		185		190			
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg							624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu							
195		200		205			
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc							672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe							
210		215		220			
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc							720
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser							
225		230		235		240	
gga ctc aga tct cga gcc atg gac gaa ctg ttc ccc ctc atc ttc ccg							768
Gly Leu Arg Ser Arg Ala Met Asp Glu Phe Pro Leu Ile Phe Pro							
245		250		255			
gca gag cca gcc cag gcc tct ggc ccc tat gtg gag atc att gag cag							816
Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln							
260		265		270			
ccc aag cag cgg ggc atg cgc ttc cgc tac aag tgc gag ggg cgc tcc							864
Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser							
275		280		285			
gcg ggc agc atc cca ggc gag agg agc aca gat acc acc aag acc cac							912
Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr Lys Thr His							
290		295		300			
ccc acc atc aag atc aat ggc tac aca gga cca ggg aca gtg cgc atc							960
Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile							
305		310		315		320	
tcc ctg gtc acc aag gac cct cct cac cgg cct cac ccc cac gag ctt							1008
Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro His Glu Leu							
325		330		335			
gta gga aag gac tgc cgg gat ggc ttc tat gag gct gag ctc tgc ccg							1056
Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro							
340		345		350			
gac cgc tgc atc cac agt ttc cag aac ctg gga atc cag tgt gtg aag							1104
Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys							
355		360		365			
aag cgg gac ctg gag cag gct atc agt cag cgc atc cag acc aac aac							1152
Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn							

370	375	380	
aac ccc ttc caa gtt cct	ata gaa gag cag cgt	ggg gac tac gac ctg	1200
Asn Pro Phe Gln Val Pro	Ile Glu Glu Gln Arg Gly	Asp Tyr Asp Leu	
385	390	395	400
aat gct gtg cgg ctg tgc	ttc cag gtg aca gtg	cgg gac cca tca ggc	1248
Asn Ala Val Arg Leu Cys	Phe Gln Val Thr Val	Arg Asp Pro Ser Gly	
405	410	415	
agg ccc ctg cgc cct gtc	ctt cct cat ccc atc	ttt gac aat	1296
Arg Pro Leu Arg Leu Pro	Pro Val Leu Pro His	Pro Ile Phe Asp Asn	
420	425	430	
cgt gcc ccc aac act gcc	gag ctg aag atc tgc	cga gtg aac cga aac	1344
Arg Ala Pro Asn Thr Ala	Glu Leu Lys Ile Cys	Arg Val Asn Arg Asn	
435	440	445	
tct ggc agc tgc ctg ggt	ggg gat gag atc ttc	cta ctg tgt gac aag	1392
Ser Gly Ser Cys Leu Gly	Gly Asp Glu Ile Phe	Leu Leu Cys Asp Lys	
450	455	460	
gtg cag aaa gag gac att	gag gtg tat ttc acg	gga cca ggc tgg gag	1440
Val Gln Lys Glu Asp Ile	Glu Val Tyr Phe Thr	Gly Pro Gly Trp Glu	
465	470	475	480
gcc cga ggc tcc ttt tcg	caa gct gat gtg cac	cga caa gtg gcc att	1488
Ala Arg Gly Ser Phe Ser	Gln Ala Asp Val His	Arg Gln Val Ala Ile	
485	490	495	
gtg ttc cgg acc cct ccc	tac gca gac ccc agc	ctg cag gct cct gtg	1536
Val Phe Arg Thr Pro Pro	Tyr Ala Asp Pro Ser	Leu Gln Ala Pro Val	
500	505	510	
cgt gtc tcc atg cag ctg	cgg cgg cct tcc gac	cgg gag ctg agt gag	1584
Arg Val Ser Met Gln Leu	Arg Arg Pro Ser Asp	Arg Glu Leu Ser Glu	
515	520	525	
ccc atg gaa ttc cag tac	ctg cca gat aca gac	gat cgt cac cgg att	1632
Pro Met Glu Phe Gln Tyr	Leu Pro Asp Thr Asp	Arg His Arg Ile	
530	535	540	
gag gag aaa cgt aaa agg	aca tat gag acc ttc	aag agc atc atg aag	1680
Glu Glu Lys Arg Lys Arg	Thr Tyr Glu Thr Phe	Lys Ser Ile Met Lys	
545	550	555	560
aag agt cct ttc agc gga	ccc acc gac ccc cgg	cct cca cct cga cgc	1728
Lys Ser Pro Phe Ser Gly	Pro Thr Asp Pro Arg	Pro Pro Pro Arg Arg	
565	570	575	
att gct gtg cct tcc cgc	agc tca gct tct gtc	ccc aag cca gca ccc	1776
Ile Ala Val Pro Ser Arg	Ser Ser Ala Ser Val	Pro Lys Pro Ala Pro	
580	585	590	
cag ccc tat ccc ttt acg	tca tcc ctg agc acc	atc aac tat gat gag	1824
Gln Pro Tyr Pro Phe Thr	Ser Ser Leu Ser Thr	Ile Asn Tyr Asp Glu	
595	600	605	
ttt ccc acc atg gtg ttt	cct tct ggg cag atc	agc cag gcc tcg gcc	1872
Phe Pro Thr Met Val Phe	Pro Ser Gly Gln Ile	Ser Gln Ala Ser Ala	
610	615	620	
ttg gcc ccg gcc cct ccc	caa gtc ctg ccc cag	gct cca gcc cct gcc	1920
Leu Ala Pro Ala Pro Pro	Gln Val Leu Pro Gln	Ala Pro Ala Pro Ala	
625	630	635	640
cct gct cca gcc atg gta	tca gct ctg gcc cag	gcc cca gcc cct gtc	1968
Pro Ala Pro Ala Met Val	Ser Ala Leu Ala Gln	Ala Pro Ala Pro Val	
645	650	655	
cca gtc cta gcc cca ggc	cct cct cag gct gtg	gcc cca cct gcc ccc	2016
Pro Val Leu Ala Pro Gly	Pro Pro Gln Ala Val	Ala Pro Pro Ala Pro	
660	665	670	
aag ccc acc cag gct ggg	gaa gga acg ctg tca	gag gcc ctg ctg cag	2064
Lys Pro Thr Gln Ala Gly	Glu Gly Thr Leu Ser	Glu Ala Leu Leu Gln	
675	680	685	
ctg cag ttt gat gat gaa	gac ctg ggg gcc ttg	ctt ggc aac agc aca	2112
Leu Gln Phe Asp Asp Glu	Asp Leu Gly Ala Leu	Leu Gly Asn Ser Thr	
690	695	700	
gac cca gct gtg ttc aca	gac ctg gca tcc gtc	gac aac tcc gag ttt	2160
Asp Pro Ala Val Phe Thr	Asp Leu Ala Ser Val	Asp Asn Ser Glu Phe	



705		710		715		720	
cag cag ctg ctg aac cag ggc ata cct gtg gcc ccc cac aca act gag							2208
Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu							
	725		730		735		
ccc atg ctg atg gag tac cct gag gct ata act cgc cta gtg aca ggg							2256
Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly							
	740		745		750		
gcc cag agg ccc ccc gac cca gct cct gct cca ctg ggg gcc ccg ggg							2304
Ala Gln Arg Pro Pro Asp Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly							
	755		760		765		
ctc ccc aat ggc ctc ctt tca gga gat gaa gac ttc tcc tcc att gcg							2352
Leu Pro Asn Gly Leu Leu Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala							
	770		775		780		
gac atg gac ttc tca gcc ctg ctg agt cag atc agc tcc taa							2394
Asp Met Asp Phe Ser Ala Leu Leu Ser Gln Ile Ser Ser							
785	790		795				

<210> 143

<211> 797

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFP-NFkappaB fusion

<400> 143

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile				35			40						45						
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr				50		55						60							
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys				65		70			75					80					
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu				85			90						95						
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				100			105						110						
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				115			120						125						
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				130			135						140						
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn				145		150			155					160					
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser				165			170							175					
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly				180			185						190						
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu				195			200						205						
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe				210			215						220						
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser				225			230					235							

Gly Leu Arg Ser Arg Ala Met Asp Glu Leu Phe Pro Leu Ile Phe Pro  
 245 250 255  
 Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln  
 260 265 270  
 Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser  
 275 280 285  
 Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr Lys Thr His  
 290 295 300  
 Pro Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile  
 305 310 315 320  
 Ser Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro His Glu Leu  
 325 330 335  
 Val Gly Lys Asp Cys Arg Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro  
 340 345 350  
 Asp Arg Cys Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys  
 355 360 365  
 Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn  
 370 375 380  
 Asn Pro Phe Gln Val Pro Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu  
 385 390 395 400  
 Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp Pro Ser Gly  
 405 410 415  
 Arg Pro Leu Arg Leu Pro Pro Val Leu Pro His Pro Ile Phe Asp Asn  
 420 425 430  
 Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn  
 435 440 445  
 Ser Gly Ser Cys Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys  
 450 455 460  
 Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu  
 465 470 475 480  
 Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile  
 485 490 495  
 Val Phe Arg Thr Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val  
 500 505 510  
 Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu  
 515 520 525  
 Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile  
 530 535 540  
 Glu Glu Lys Arg Lys Arg Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys  
 545 550 555 560  
 Lys Ser Pro Phe Ser Gly Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg  
 565 570 575  
 Ile Ala Val Pro Ser Arg Ser Ser Ala Ser Val Pro Lys Pro Ala Pro  
 580 585 590  
 Gln Pro Tyr Pro Phe Thr Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu  
 595 600 605  
 Phe Pro Thr Met Val Phe Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala  
 610 615 620  
 Leu Ala Pro Ala Pro Pro Gln Val Leu Pro Gln Ala Pro Ala Pro Ala  
 625 630 635 640  
 Pro Ala Pro Ala Met Val Ser Ala Leu Ala Gln Ala Pro Ala Pro Val  
 645 650 655  
 Pro Val Leu Ala Pro Gly Pro Pro Gln Ala Val Ala Pro Pro Ala Pro  
 660 665 670  
 Lys Pro Thr Gln Ala Gly Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln  
 675 680 685  
 Leu Gln Phe Asp Asp Glu Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr  
 690 695 700  
 Asp Pro Ala Val Phe Thr Asp Leu Ala Ser Val Asp Asn Ser Glu Phe  
 705 710 715 720  
 Gln Gln Leu Leu Asn Gln Gly Ile Pro Val Ala Pro His Thr Thr Glu  
 725 730 735  
 Pro Met Leu Met Glu Tyr Pro Glu Ala Ile Thr Arg Leu Val Thr Gly

			740					745					750			
Ala	Gln	Arg	Pro	Pro	Asp	Pro	Ala	Pro	Ala	Pro	Leu	Gly	Ala	Pro	Gly	
		755					760					765				
Leu	Pro	Asn	Gly	Leu	Leu	Ser	Gly	Asp	Glu	Asp	Phe	Ser	Ser	Ile	Ala	
	770					775					780					
Asp	Met	Asp	Phe	Ser	Ala	Leu	Leu	Ser	Gln	Ile	Ser	Ser				
785					790					795						